AE007028 Myrabacte AR095713 Sequence AR147694 Sequence AE007160 Myrabacte 281509 Caenothabdi 29586 Myrabacteri Z74410 Myrabacteri 295390 Myrabacteri 295390 Myrabacteri

U43540 Mycobacteri U35017 Mycobacteri AE006921 Mycobacte AF041819 Mycobacte

U35021 Mycobacteri

IB6264 Sequence 18

Post-processing:

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Scoring table:

Searched:

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AK027649 Homo sapi
AB051548 Homo sapi
AB050515 Maccaca Fa
AL360171 Homo sapi
AJ292298 K1etsiell
163424 Homo sapien
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L40027 Homo sapien
BC04783 Mus muscu
AC04688 Homo sapien
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AC036418 Homo sapi

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nassea chlamydomon

REFERENCE AUTHORS

SUMMARIES

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/ Translation=Executed
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AIVEDAJ RLVOGDI TDAELVSOLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTF
TILRAVRRHGVRLHHI STDRYYGDLELDDRARFTESTPYNPSSEYSAYRAGJOBLVRA
WYSSLCVRAT I SNCSNNYFQYGYVERFERPROTINCLFGLLKLYGDGGNVHOMIHVDDH
NSAVRRILDDRGRIGFTYLLSSEGERONLTVLRSLLERMDRDPDDFDHYVIDKVHBLRY
ALDPSRI,YDELCWAPRHTDFERALKTI IDWYRDNESWLASLKHAGGRYQDAGO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"Mreepreldvpgaweitptihudsrglffewltdigfkaraghs
Ludrgongsyssagulrglefradlpspgakyytcysgsyfbyvydiregsptfgrwds
Viludgodrniyvspglalglagfladgdnstywildsaefwrogrghtigatprtlasirkw
styggdpslisdrdaapsfeedvrrglllpggtdvsrfigemrgt"
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/note="3-4 copies in M. tuberculosis genome; Found in the rtb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv. H37Rv. Erdman, and many isolates; not found in M. smegmatis & M. avium."
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1 (bases 1 to 928).
Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K Molecular analysis of genetic differences between Mycobacterium bovis BCG and virulent M. bovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
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                                                                                                                                                                                                                                 /product="rhamnose biosynthesis protein"
/protein_id="AAB66647.1"
/db_xref="G1:2326949"
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Mycobacterium bovis deletion region 3, 5'
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/db_xref="G1:2326951"
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/transl_table-11
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/qene="rm1C"
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/db_xref="G1:2326950"
/translation="MRLLVTGGAGFIGTNFVHSAVREHPDDAVTVLDALTYAGRRESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhamnose biosynthetic genes related to a novel repeated sequence of Mycobacterium tuberculosis
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Namku, Taegu
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Namku, Taegu
                                    Hickey, Molecular Microbiology, Ave. W., Seattle, WA 98119, USA
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Virulent M. bovis has additional 10 kbp at this site"
637 c 416 g 214 t
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Bacteria; Firmicutes; Actinobacteriae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology,
Medicine, Yeungnam University, 317-1, Daemyunydong,
705-035, South Korea
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        Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, M.
PathoGenesis Corp., 201 Elliott Ave. W.,
Location/Qualifiers
                                                                                                                                  /organism="Mycobacterium bovis"
/sub_species="BGG"
/db_xref="taxon:1765"
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/clone="piSil6"
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/gene="rfbA"
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/gene="rmlB"
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/db_xref="G1:13879147"

/translation="MAYTVGYTCAIPQELAYLRGVLVDAKRQQVAQILEDSGGLDAHR
/translation="MAYTVLADREGCRTIVETGVAGGLDPELCIGDIVIANHYVCHIPF
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/rouslation="anthyl" transferase
/rouslation="anthyl" tran
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VWHCIRCGDFALGGFQGKGAPEDAPI.MRGKALROA IITRALGVERI.VKAI.VIALAAW
WWHENGROA LOATI.DRIIJVULRAACKVDOMYTIHAI.EKAILAAKISTILAI.ITGMI.A
AYAVI.QAVESVGIMI.KRWERYEAVATSIFLELEVIIII.AKGITTTRVVTFSINVAAV
VYII.ISKRLPGVRGGRKAYDVERRGKGLDLERAAMI.T"
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/protein_id "AAK443±5.1"
/db,xrcf="G1:1879146"
/fd,xrcf="G1:1879146"
/fd:Stanslation-"MKGLRVSKVTSAFFALETPARKARKAAKVNLDOVAOCKETDEG
/PLLOGICOPGSAKALTPAAWSKOSOKVPATHCRPCCAPGAAASALTCAL/ARAWSVVE
VKPAPRAATESLOSKAARESK"
/hote="similar to GB:AL009126; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to GP:145427; identified by sequence
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/product="5-methylthioadenosine
nucleosidase/S-adenosylhomocysteine nucleosidase,
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/protein_id-"AAK44321.1"
/db_xret-"G1:13879145"
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/qene="MT0099.1"
8/91, .4162
/qene="MT0099.1"
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/gene-"MT0101"
5105. .7390
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/qene-"MT0100"
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/gene="MF0100"
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/qene="MT0099"
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/gene-"MT0099"
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/gene-"MT0101"
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/qene-"MT0098"
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/dene "MT0098"
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Mycobacterium tuberculosis CDC1551.

Mycobacterium tuberculosis CDC1551.

Mycobacterium: Firmicutes; Actinobacteriaceae;

Actinomycetales; Corynebacterium tuberculosis complex.

Mycobacterium: Mycobacterium tuberculosis complex.

Mycobacterium: Mycobacterium tuberculosis complex.

Mycobacterium: Mycobacterium tuberculosis complex.

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Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gill,J., Mikula,A. anu pismarim.

Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1. 9764
I. 9764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, D., Pleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, D., Peterson, J., Bebby, R., Bodson, R., Cwinn, M., Halt, D., Hickey, E., Kolonay, J.E., Nelson, W.C., Unayam, L.A., Ernolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                         /organism="Mycobacterium bovis"
//db_xref="taxon:1765"
misc_difference replace(1400. -2928!,"")
//note="absent in related avirulent strain M. bovis BCG"
COUNT 1706 a 3191 c 2929 g 1453 t, 2 others
                Direct Submission
Submitted (29-ANG-1995) Mark J. Hickey, Molecular Microbiology,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA
Location/Qualifiers
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section 7 of 280 of the
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/strain="CDC1551"
/db_xreff"taxon:83331"
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 1; Length 9281;
Pred. No. 14;
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122. .1414
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1449. .2123
/gene="MT0096"
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AE006921 AE000516
AE006921.1 GI:13879142
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ilarity 100.0%;
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Unpublished
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Best Local Similarity
Matches 18; Conserv
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SOURCE
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Yu, S.
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VSGTVSGRAVROGRPSWIGSSSCHPNWRAARHAESI.GETAVEVEVIA.EPCGVIAVAD
KNDSARDAVAALABRGLRTMLLTGDRUPESAAAVATRVGIDEDVIADI ILPEGKVDVIEQ
LRDRGHYVAAWGDGI INGPRALARADI.GMA GGGTDVAI,GAADI ILVROHLDVVPLALD
LARATMRIVKLINWWAFGYNIAAI PVAAAGILINPLVAGGAAMAFSSFFVVSNSLRLRKF
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/protein_id="aAA44325.1"
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/translation="MLAQATTAGSFNHHASTVLQGCRCVPAAMWSEPAGAIRKHCAT1
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RPVVPPPVGREGIRRARROHEDWIWRRWALLCOFJAQIALGYOĞFCIJJVGJTHQHPT
GGTHLLNESTSWSTALGVI MVGAALWPSAAAGIAGVITAFVA ITTOVV I VOALSGAV
STTRILTHLPVVIGAVLA INWARSASOBRPREPDAVABPDIVIPDNASKGKRRGHLWP
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/translation="MDWLHPHGDLTFFERARKRG17LSNQQY146MSRG.SGY1.7PQARA
                                                                                                                                                       /db_xref="G1:13879148"
/translation="MTTAVTGEHHASVQRIQLRISGMSCSACAHRVESTLNKLPGVRA
AVNFGTRVATIDTSEAVDAAALCQAVRRAGYQADICTDDGRSASDPDADAHARQLLIRL
                                                                                                                                                                                                                                AJAAVLEVPVADLSVWEGVVPATRETGWQWVLSALALPVVTWAAWPFHRVAMRNARHH
AASMETLISVGITAATIWSLYTVFGNHSPIERSGIWQALLGSDAIYFEVAAGVTVFVL
VGRYFEARAKSQAGSALRALAALSAKEVAVLLPDGSEMVIPADELKEQORFVVRPGQI
                                                                                                                                                                                                                                                                                                         VAAOGLAVOGSAAVDMSAMTGEAKPTRVRPGGQVIGGTTVLDGRLIVEAAAVGADTQF
AGMVRLVEQAQAQKADAQRLADRISSVFVPAVLVIAALTAAGMLIAGGQPDRAVSAAL
AVLVIACPCALGLATPTAMMVASGRGAQLGIPLKGYKSLEATRAVDTVVFDKTGTLTT
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GKLGGHNGLPVSIVVTTTLTDLQTGAGKGFTGGGTLLIAMADV1RWTSHAHHYSPASGR
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TGRTDITELTLACGPDNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQPRYNTFHHPERF
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3103 c 3360 g 1748 t
/note="similar to SP:P46840 PID:559912; identified by sequence similarity; putative"
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                                                                                                 /product="cation-transporting ATPase, El-E2 family"
/protein_id="AAK44324.1"
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/protein id="AAK44326 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRYPLGCGTVGGPQMTAPSSA" complement(7337. .8185)
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/gene="MT0103"
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/transl_table=11
                                                        /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0102"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9236 ACATCAAAGTGATTCGCG 9219
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ITAK LIVUT TPAGLIDTYFESINGSVSVEVAAKHALDYWKGGLICK KREIMTWKGGYHGD
TEK LIVUT TPAGLIDTYFESINGSVSVEVAAKHALDYWKGGLICK KREIMTWKGGYHGD
TEHAMSI COBHIGGHISLMTDVIAAQVYPAQVYRDYDPAYSAAFAGLICHAHACHIAAV
VEPVVQGAGGARFINDFRULIDLICKRYEVLLIFDELATGFGHTGALFAANHAGVST
DI MCVGKALTGGYLSLAATLCTADVAHTISAGAAGALMIGPTFMANPLACAVSVASVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MICSGVNPPVAAAMEIEGNAATPRPIPVTVAKTSALGEHACMAPPNOPEDTQDDAGTESRSALDEDDEKTPPRVLTLRIAPWDVCTVVILAVELVWVTMTSWESKLFAFTONVCPPDAGPLVPFGVNYYIYPVWWGGIGAAIATAVIGEFVSALKGWYM
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                                                                                   putalive 8 amino-7-oxonomanoate synthase (bioF), putative dethiobiotin synthetase (bioD), and biotin synthetase (bioD)
                                                                                                                                                                                                                                                                                                                   Bacteria; Firmleutes: Actinobacteria, Actinobacteridae; Actinomycetules: Ocyvebacterineae; Mycobacteriaceae; Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium tuberculosis complex.

1 (bases 1 to 10019)
14. S. and Jacobs, W.R. Jr.
Clouting, sequencing, and identification of Mycobacterium bovis BCG biotin biosynthetic quees by complementing two Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
                                                          adenosylmethionine-8-amino-7 oxononanoate aminotransterase (bioA),
18-JAN-1948
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/note "ORE2; similar to MrcY336.36"
/codon Start 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(259. .1048)
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   BCT
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AF041819 10019 bp DNA
Mycobacterium bovis BCG putative
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/roduct="unknown"
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1810. 317.
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/gene="bioA"
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SOURCE
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CGPHLAPAPMANSLPGQWTAHVTLARRVGGHQLGRALRIAGRPSK!!R:RFAGLRRWDG
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CLVRRIPAOCHTLINOLDTQASEEELGGTLCCALANRLRTTRFDAAN, HADAADLGPR
RALTGEPLAPOLTATATAGNGGLIGEAHIKVIKALFRPPARKGGCVHIPVGRESRPGRG
SRSISSRRAGPLRPAGHGLATPHKRPTKPQTRHHPEQPAIKHVTAKWLPDPPS
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BELOGHOGLPYSIVYTTLTDLDGTGARGFTGGGTLLJMADVY IRMTSHAHYSPASGR
YPQAIFDHGTPLALYHTKLASAQQRIMLFANDRGCTKPGCDAPAYHSOAHHYTGWTS
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LDRGVWLRPFRNLVYAMPPYICTPAEITQITSAMVEVARLVGSLP"
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4277. .4957
/gene="bioD"
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/note="bioD; similar to MTCY336.33c"
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/producin_id "Angustan..."
/db_xref="G1:2791853"
/db_xref="G1
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NFFTappmligli.svlavvasalmwgwrehrgpgwyaglsiglftaaataagggluvy
RLKYGALDFDTVPLSKGDHALTYVTQAPPVFFARRPLQIALTLMWPAGTASLVYALLA
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/note-"ORF10; similar to MTCX336.13c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"ORF11; similar to MTCY336.12"
/codon_start-3
                                                                                                                      /note-"BioB; similar to MTCY336.15c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
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                                                                                                                                                                                                                                     /transl_table 11
/product-"biotin synthetase"
/protein_id+"AAB96962.1"
/db_xref="G1:2791851"
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1 (bases 1 to 12412)
Stover,C.Kendall and Mahairas,G.G.
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/product="unknown"
/protein_id="AAB96963.1"
/db_xref="G1:2791852"
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/product="unknown"
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186264
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/qene-"biob"
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9

ACCESSION

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VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS JOURNAL

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FEATURES

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/product="conserved hypothetical protein"
/product="conserved hypothetical protein"
/protein_id="AAK45896.1"
/protein_id="AAK45896.1"
/protein_id="Conserved"
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/protein_id-"AAK45893.1"
/db_xref="G1:13H81254"
/translation-"MYEUVAGKORAPVAAGVYNVYTGELABYATPTAARM:1.EPPRFC
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                                                                                                                                                                                                                         Zonce "similar to GP:1680650; identified by sequence similarity; putative"
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/protein_id-"AAK45894.1"
/db_xref-"G1:13881255"
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/codon_start-1
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/protein_id="AAK45895.1"
/db_xref="G1:13881256"
                                                                                                                                                                                                                                                                                                                                                            /product-"biotin synthase"
/protein_id-"AAN45892.1"
/db_xref="G1:13881253"
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/ tene "MIT62/"
complement (395) (4054)
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/gene="MT1628"
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Zqene-"MT1625"
2997. .3236
Zqene-"MT1625"
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Zurne "MP1626"
1317. .3898
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/qene-"Mf1626"
                                                                                                                            /qene-"MT1624"
1947. .2996
                                                                                                                                                                                            /qene="MT1624"
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CLVRRLPAVGHTLINOLDTOASEEELGGTI,CCALANNI,RTRENAAL,RIANDADLGPR
RALTGEPLAPOLTATATAQROGLIGHAHIKVIRALFRPPARKGGCVIIPYGKKSRPGRO
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AHHYSPASGRYPQAIFDHGTPLALYHTKRLASPAQRIMLFANDRGCTKPGCDAPAYHS
QAHHYTAWTSTGRTDITDLTLACDPDNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQPR
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1 (bases 1 to 1778)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, M., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzbergy, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 17783)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpcuter,L., While,O.,
Peterson,J., DebGy,R., Dodson,R., Gwinn,M., Haif,D., Hirkey,E.,
Kolonay,J.F., Nelson,W.C., (Unmyum,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
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                                                                Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

    17783
/organism="Mycobacterium tuberculosis CDC1551"

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Submitted (25-APR-2001) The Institute for Genomic
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
                                                                Indels
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Mismatches
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complement(831. .1499)
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Query Match
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LOCUS
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KEYWORDS
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SVQRNIEIGHFGGGE"
7468.
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WAGAVSDLEFIGFHPPMLFAGRAGGRRPLIFPBATGEGGLIUVDROGHSTGDGTHPMG
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VVPGAHYSGGIVTDVYGQTELLGLYAAGEVARTGLHGANRLASNSLLEGLVVGGRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to SP:P11458 GB:X12713 PID:581137 GB:U00096 PID:1651334; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAGPAWRDADDVVIGTGVAGLAAALAADRAGKSVVVLSKAAQT
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FGDTKLGSAVPTPPVLIVQAVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSL
HPLSAPMTLRWLTDRFAGKPLTDHRVRTTWPTIFNPMTYAGMARLAVIAAKVITGRKL
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/gene="MT1631"
7468 9051
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/note="similar to GP:608530; identified by sequence
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                                                                                                                                               /note="identified by Glimmer2; putative"
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                                                               complement(5660. .6193)
                                                                                                       complement(5660. .6193)
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6419. .7468
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9021. .9908
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Matches 18; Conserv
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section 246 of 280 of the
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            08-SEP-2000
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                                                                                                                                                    DNA molecule encoding for cellular uptake of mycobacterium tuberculosis and uses thereof Patent: Us 6008201-A 1 28-DEC-1999; Location/Oualifiers
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Pred. No. 95;
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                                                                                                                                                                                                                                                                                                Score 16.4; DE
Pred. No. 95;
0; Mismatches
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Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Mycobacterium tuberculosis CDC1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR147694 1535 bp DNA
Sequence | from patent US 6224881.
AR147694
акиу6713 1535 bp DNA
Sequence 1 from patent US 6008201.
AR096713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"unknown"
                                                                                                                                                                                                                           /organism-"unknown"
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                                                                                                                                                                                                                                          458
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Riley, L.W. and Chong, P.
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                                                      AR096713.1 GI:10025749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR147694.1 GI:15111784
                                                                                                                                                                                                                                                                                                  91.1%;
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Riley, L.W.
                                                                                                                                                                                                                                                                                                                                                                       841 ACGTCAAAGTGATTCGCG 858
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Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome.
AE007160 AE000516
AE007160.1 GI:138
                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                 . 1535
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KEYWORDS
SOURCE
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LGTCHVCHQDFERPDMLACQTHGAHVCSLCLSTDKQAEHVLPGLARAHIFGLOVP"
romptlement (3485. 4378)
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FGLARELNVERGGTGSPRAADHTASFALDIDDLDLTVRSGYNCIKKEGVIFVGELV
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                                                                                                                                                                                                                                                                                                  /LTAINS I AT 1010-**MMPGV1TNSESPTAADHDRITATRETLEDYTLRLAPRSYRRWPP
AVOGT SALGGTAYLADFA1GANVGTTWGTAANLCGTALFALVVWTVGLPLAYYAARYN
11) LDL 17RGSGFGYTGSVTWVIFATFFTFIFFALEGSIMAQGIRLALHIPIMAGYACS
11) I FPLVVYCMKVI,SQLGJMTTPLMLILMAAPFGYLVVSHPDSIGGFFSYGGREGGGG
G1.SFGSVLLAAGVTLSLLAQIAEQ1DYLRFMPPRTPENANKWWTWTLLAGGGWVAFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MSLTRKPPRSPPQRPPRISGVVRLRLDIAYDGTDFAGWAAQVGQ
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PID:1788657; identified by sequence similarity; putative"
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similarity; putative"
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                                                                      /note-"identified by Glimmer2; putative"
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/qene="MT3563"
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/gene="MT3563"
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                                 /gene-"MT3561"
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DDHIAAIALFGNPSGRAGGLMSALTPQFGSKTINLCNNGDPICSDGNRWRAH.GYVPG
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                                                                                                                                            Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Closes I to 16384)
Fleischmann, N.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-ARR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
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Firmicutes; Actinobacteria; Actinobacteridae;
                                     Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/db_xref="GI:13883391"
                                                                          Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 16384)
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JOURNAL
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AUTHORS
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/Lrānsialialion-"MTRINI/ULFLSSLAVCTYSQTMTKTIIDFCSPSEPNSCGPGGKC
MELSJGNRCDCPFGLMGRRCQRPCQDYKSCARMKSEBRCHWTRPISPFADNY/ALSC
GQCKNNGKQDLALIPPILDHIBWFVGRMESKTSAHHRFPEPNSGPYREILIJWU ISEVU
SEDREPVNI SYRAM-LIJGTTNYHVBEGELT/SREPHEDYGEVELINRPDHGIBILS FELVY
NYGLMLIBEGTVKGTQIRLETKYKKGMAGVFRBEIVKSKRMFNI,INANSI,EERVVWVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true left end of clone F2IA3 is at 1 in this sequence. The true right end of clone F2IA3 is at 6434 in sequence 281071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The end of this sequence (41993, .42096) overlaps with the start of sequence 281071.
                                                                                                                                                                          Submitted (06-NOV-1996) Nematode Sequencing Project, Sanger Centre, Ilinxton, Cambridge CB10 RQ, England and Department of Genetics, Washington University, St. Lewis, MO 63110, USA. E-mail: Jesssanger.ac.uk or revenementede.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         start of this sequence (1. .104) overlaps with the end of sequence 281463.
                                                                                                                                                                                                                                                                          On Jul 24, 1997 this sequence version replaced gi:1695020.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seg/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone F21A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                            available information. Current sequence finishing criteria for the C. elegans quenome sequencing consortium are that all bases are cither sequenced unambiguously on both strands, or on a single strand with both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true left end of clone F28F8 is at 31993 in this sequence.
The C.elegans Seguencing Consortium.

Erratum:[[pub]ished errata appear in Science 1999 Jan 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep 3;285(5433):14931].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to EGF-domain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /crganism."Cacnonhabditis elegans"
/db_xret-"Laxon:6239"
/chromosome-"V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted using tWMAscan-SE-1.11
prediminary prediction
similar to tWMA Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agene="F21A3.Ll"
/note="CAT Mot M-LENA
/note="CAT Mot M-LENA
predicted using tRNAscan-SE-1.11
preliminary prediction
similar to (ENA-Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:017829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id-"CAB04157.1"
/db_xref="G1:3876159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(216, .288)
/qene."F21A4.t2"
/note "CAC Val V tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (219. . . 288)
/qene "F21A3.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /vene-"F21A3.11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone-"F21A3"
                                                                                                     10 32096)
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                                                                                                                                                    Direct Submission
                                                                                                       2 (bases 1 to
McMurray, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             name- F21A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                               AUTHORS
TITLE
JOURNAL
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                                                                                                             REFERENCE
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       REMARK
                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="ribosomal protein S11"
/product="ribosomal protein S11"
/db_xxef="G1:1883398"
/translation="MPPAKKGPATSARKCOKTRREKKNVPHGAAH KSTFNNT1VTI
/progNav1PaASSGHVGFKGSRKSTPFAAQLAAENAARAQDHGVKVVDVFVKGPGSG
RETARSLQAAGLEVGAISDVTPQPHNGVRPFKRKV"
complement(129..7503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="marlvgvdlprdkrmevaltyledickreneilaatgidkulk
trdlteeqlihlrdyleanlkvegdlrrevqadlrkkieliccyqchikhkrmbvkqqr
                                                                                                                                                          /translation="marytgputrksrkijrtdi.vggiodafekrpyppcghgrafikes
Eytloloekokarfytgvmekofrkyyeeavropgkytgeelilkii.esri.Dnvjyragi
artrrmarqlushghfnvngvhynvpsyrvsqydjvivroxslnyvpeqiaketager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7129. .7503)
/gene="MT3567"
/note="similar to GP:2104383; identified by stapmence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seducince
                                                                                                                                                                                                                                                                                                                                                               /iote="similar to SP:P45812; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.18; Score 16.4; DB 1; Length 16484; 94.48; Pred, No. 1.3e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEF21A3 32096 bp DNA INV 25-UC
Caenorhabditis elegans cosmid F21A3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7719. .7832)
/gene="MT3567.1"
/note="similar to SP:P45810; identified by similarity; putative"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                    PIPSWLQVYGERQRVLIHQLPERAQIDVPLTEQLIVEYYSK" complement(6706. .7125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity; putative"
/codon_start=1
/transl_table=1
/product='ribosomal protein S13"
/protein_id='AAK47906.1"
/db_xref="G1:13883399"
                                                                                                          /protein_id="AAK47904.1"
/db_xref="G1:13883397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7719. .7832)
/gene="MT3567.1"
                                                                                                                                                                                                                                                                                                                 complement(6706. .7125)
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                                                                                                                                                                                                                                                                                                                                                                                               similarity, putative" /codon_start=1
             putative"
                                                                                                                                                                                                                                                                                                                                         /gene="MT3566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MT3567"
                                                                                                                                                                                                                                                                                       /gene="MT3566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 11346 ACGTCAAAGTGATTCGCG 11363
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us-09-785-904-3.rge

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/rodon_start_1
/rodon
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Actinomycerales; Corynebacteriae; Mycobacteriacea;
Mycobacterium: Mycobacterium tuberculosis complex.

1 (bases 1 to 3247)
Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Colloor,R., Badcock,K., Basham,D., Brown,D., Chillinyworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quall,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Barrell,B.G.
                                                                                                                                                                   PEFTNKVEQQ IDVDVWFDTALRNFAKIILKVAK EEQEKLLEKLPVKGGAMPPKGPKAGAQ
TSTVANYKG TIDDFYK I VCSGRPAWALHWRDVMLDWDKLLENTPFFSKMFFAY EKHQKS
LETSERMERLQATKEIITTVWKNHTEFEMAKNQAAI VEYLMPEHEAKEEPTDKKKDPEE
                                     INNHVEFMVVRIRAGFTLHULLKCLSSDKMSVTTASFLAVDMISATETLSASGWVLRN
FDSKQWMLDIKTRQFYLADATDITVSSDKRHRAIDETHLKTAESTUTHWKTGDLIYAP
                                                                                                                                  RSFVDRDQSHRWTELDMMEMMLYVLYDWTHGKLPWKSSKSRERIMEMKFLFTENLQKE
                                                                                                                                                                                                                                                                                                           EAAAAVVGKKRRGRKPKKEDDPKMELKDEVKDLKDFVVEGTQVTEFSKSRLHMSGKRF
                                                                                                                                                                                                                                                                                                                                                                            comptement(join(27870. .28389,28450. .28539,28591. .28708,
29358. .29380))
/qone "F21A3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comploment(join(27870. .28389,28450. .28519,2859). .28708,
29458. .29580))
/qene="F21A3.6"
GAAYCYI,VCDKPCKKFG11,YLE1GEDNVTT1ANQVDFYHQOSS1,GYSHKFSAL,1DAG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mode="predicted using Genefinder wheak similarity to Shark myoglobin (SW:P02206), contains similarity to Plan domain: PF00042 (Globin), Score-39.5, E-value=1.50-10, N×1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2001
segment 70/162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 3; Length 32096; Pred. No. 1.5e+02;
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Mycobacterium tuberculosis H37Rv complete genome;
295586 AL123456
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                                                                                                                                                                                                                                                                                                                                                                       FIFTNCRNWNCRFAEYAGKLANCG1"
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94.4%;
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Matches 17; Conservative
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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26204. .26320,27040. .27510)
/gene="F21A3.5"
join(22967. .23146,23217. .23582,24576. .24916,26030. .26153,
26204. .20320,27040. .27510)
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/gene="F21A3.4"
join(21375. .21425,21480. .21710 22206. .22358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(21375. 21425,21480. 21710,22206. .224%8,22411. .22695)
/gene="P21A3.4"
/note="predicted using Genetinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="witton" with the propertion of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MOITKV REKITLTSITSESVAFY EHDVDFCCRLLEHKLELEME
KKLOLSNRIDOVOSOYTELWDRYDKARREESDISCRYTAWACHLSEWMNEVKLKKAKM
GTWEISATLSAELOESLDLLAEKRVIVORNEESIDYRRHLIKQOLKDLKLDCDREEE
KCEYWNDKAAEIEKVVEMIKEQORKSIGERVEEKRMODEOKKMLEELEMLLKKTGKKR
QILDENANLVASFSSLTEESS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOMCHNKWEWLTLLIMSASLDLSFGFLVIPFWYOPVIAGYSIGILNGFGVPLRVWYYI
CVVQIAGVTVSVCALFFETRFFLLYAKOSCWKHLRRPWLILNYTICVVYMIPTYLSIPD
CYTGRAYOFSKYPCLPOEVYDEKVFLTTWSTGSTAYNMSPLTANOOTLIFVFLIYWNM
RKSWVEVKMSKRTLDMHRTFLKTILIQVIPLITVMGPLMINFFT IYNSYNGGANUL
SISMMATHGLVSSLAMIYLHKSYWATLLQLLSPKFIFEDRETMHFSKYHQHPOGPS'
complement (join (15549. 15743,15934. 16071,16247. 16444,
16540. 16559,16681. 16823,16995. 17181,17233. 17415,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(15549. .15743,15934. .16071,16247. .16444,
16540. .16598.16681. .16823,16995. .17181,17233. .17415,
17532. .17703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:017826"
/translation="MCMNTSPAKFLDTPQFLSTTMYTITIIGLPVHIFGGLCVVFKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity to Aspergillus acid phosphatase (TR:Q12546) cDNA EST yk3g4.5 comes from this gene cDNA EST yk69f10.5 comes from this gene cDNA EST yk29f10.5 comes from this gene cDNA EST yk285e4.5 comes from this gene cDNA EST yk55a5.5 comes from this gene
                                                                                                                                                                                                                                                  /note="predicted using Genefinder
contains similarity to Pfam domain: PF01604 (7TM
chemoreceptor), Score=254.2, E-value=5.6e-73, N=1"
                                                                                                                Join(14078. .14402,14665. .15074,15212. .15475)
/gene=F21A3.1"
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                            e-"predicted using Genefinder
similarity to protein kinases"
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/gene="F21A3.2"
/note="predicted using Genelinder
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/db_xref="GI:3876157"
/db_xref="SPTREMBL:017827"
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/db_xref="G1:3876155"
/db_xref="SPTREMBD:017825"
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available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old been renumbered from the original cosmid submissions but the old peen rediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDGVKEPPGPAALVPVGGATMLMILAGANRQCHPGTRDRELPLUNRILLATAPLVALGAMA
YSWYLMHWPLLIFWLSYTGHRHANNYBGAAVLLVSGLLAYTTRIJVEDPLRYRAPGAY
SRDAAVPPIP PWRRIERRPYTIVGSVYALGVALTATSFTWREHY IVORAGGELSGLS
SRDAYGARALIDHYWPKLRNRPTLLEVRHDLPTSTROGGISDFVWRAIINGTYGDVD
APRTIALAGGSHAEHWLTALDLLGRWHHFKVYTYLKMGCPLSTESPPLINGNNAPYPO
GHWVQAAMAKLVADHPDYVTTSTRYNIKFGDWPATYVGIUWGTFADNNIPVLAMR
DTPWLYKDGOPFIPADCLAKGGNPGSCGIAREKVLVINKNPTILDYVAKFPLIKFDLDMS
AICRTDTCRAVEGNVLYYRDSHHLTPTYMRTMISELGRQIAANTIWW"
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LVAVPHVWFGRVSGGVDVFTALSGFFFGGKILRAALNPDLSLSPIAEVIRLIRRLLPA
LVAVLAGGALLTAIAPQPTRWEAFNORSLASLGYVNWELASTVSNYLRAGEAVSPLQ
HIWSMSVOGGFTLAFLLVAGGAYLLRRLFRGPRAPYLRTMFVVLLSTLTLASFIYAI
VAHHAYQATAYYNTFARAWELLAGALVGAVVPHVRWPWMLRTAVATAALAAILSCGAL
                                                                                                                                            Direct Submission
Submitted on behalf of the hycobacterium
Submitted (1.300-1998) Submitted on behalf of the Wellcome
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique
Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
Ou Jun 27, 1998 this sequence version replaced gi:2117233.
                                                                                                                                                                                                                                                                                                                                                                                            \ensuremath{\mathsf{N}}^{\mathsf{C}} \cdot \ensuremath{\mathsf{G}} = \ensuremath{\mathsf{S}} . Tuberculosis sequencing at the Sanger Centre are Details of M. tuberculosis sequencing
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/strain="H37Rv"
/db_xref="taxon:83332"
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/strain="H37Rv"
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/strain="H37kv"
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   Nature. 393 (6685), 537-544 (1998)
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/gene="Rv1565c"
/gene="Rv15655c"
/note="Rv15655c"
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33. .32091
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1. .32437
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complement(39.
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                                                                       (bases 1 to 32437)
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                                                                                                                  Parkhill, J.
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                                                                                                               AUTHORS
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/translation="MANAATGGITPEOTIAVDGAHLWHPYSSIGREAVSPVVAVAAHGA WITLIRDGQPIEVLDAMSSWWTAIHGHGHPALDQALTTQULRWMHWHEGGLTHEFAAR WITLIRDGQPIEVLDAMSSWWTAIHGHGHPALDQALTTQULRWMHWHEGGLTHEFAAR TELLAWSIGDPHIGGWHSTWYDVLAAQVFAARWALQWRGRGLPGRRRLMTWRGGYHGU TELAWSIGDPHIGGWHSTWYDVLAAQVFAPQVPRDYDPAYSAAFEAGLAQUNGGAGGWRFHDPRYLHDLRDICRRYEVLLIFDEIATGFGRFTGALIFAANHAGYSP DIMCVGRAATGGYALTGGADAWHTISAGAAGALWHGPFFWANHIACAYSVASVE INLAGOWWRTHTELAAGLTAGLDTARALPAYTDVRVGGAGAHWHGPFFWANHIACAYSVASVE DIDRGWWRTHTELAAGLTAGLDTARALPAYTDVRVGGAIGYHEGPFWANHIACAYSVASVE DIDRGWWRTHTELAAGLTAGLDTARALPAYTDVRVGGAIGYHEGSLPWANHAATPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"SPTREMBL:006623"
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AALATAVIGPEVSMLKGWYMSFWPLISIAVITVTSIAGYALAGFSERYWH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Translation«"MKKSMKSOSFAIGLAMMLAPMVAAPGLAAADPATRPVDYQOTTD
VVIARGLSQKGVPFSWAGGGISGPTRGTGTGINTVGFDASGLIQYAYAGAGIKLPRSS
GQMYKVGQKVLPQQARKGDLIFYGPFGTQSVALYLGKGQMLFYGDVVQVSPVRTNGMT
FYLVRVLGTGTGVPTFVQQAFVQDAPVQQAPVQQAPVQQAFVQQAFVQQAP
                                                                                         probably exported has QOAPV repeats at C-terminus, similar
                                                                                                        to hypothetical M. leprae protein, to putative invasins 1,2(007390, 007391) from M. avium and slightly similar to creminus of Listeria invasion-associated protein p60 precursor P60_LISMO P21171. FASTA results, 04634 COSMID H170 (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlap. Thearst scoreis 0.890"
complement(2327. .3019)
/ucne-"Rv1566c"
/uote-"Rv1566c, (MTCY336.37), len: 230. Fun tion: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /hote-"Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse
score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3030. 3036)
/mote-"possible RHS, AAGCAGG, for Rv1566c"
complement (3258. 3263)
/mote-"ASNI site: ATTAAT; probably linking fraqments
[44/G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PS00600 Aminotransferases class-III
pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /iransl_table 11
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/protein_id-"CAM09071.1"
/db_xref-"G1:2117271"
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complement (3259. .3543)
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/qeue-"bioA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / I rais lation - "MSY LAGAAQ IGGYMYGAPLY I CMTROVKARWEURAGAGLLOPWR DILLKOLGKOO I TPAGYT I VEAAAPV I VAGTTLLIAA I APLVATGSPILDSADLEAVYO LAFLOTYALITLAG I DYGYSPGGMGASERITTABALVEPT I LLAVYALIS I PAGSANLGAL VAST I DHPGHYVSI AGVLEVI VI VI VAETGRLEVINPATHI, ELITWHEAMYLEY AG PRI ALVEWAAGNMI, TY LIALLANLE I BMG I AGAAPTALDY ITGVVAVAAK VA I LAVIL ATFEVELAK, RI FRYPELI, AGSFLI, ALLAVTAANFTYGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HY:D_ECOLI P16430 formate hydrogenlyase subunit 4 (307 aa) FASTA scores, opt: 570, z-score: 591.6, E(): 2-1e-26, (37.8% identity in 305 aa overlap) and NUOH_ECOLI P33603nadh dehydrogenase i chain h (325 aa) FASTA scores, opt: 207, z-score:220.7, E(): 9.5e-06, (26.5% identity in 26.3% adoverlap)
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gl:1409752.
                                                                                                                                               Details of M. Luberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(Wile, http://www.sanger.ac.uk/Projects/M_tuberculosis/) GDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TH yeues implemented in Tbyarse (Kroqh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position 6 + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /_ore="Rv0085, (MTCY251.03), len: 220. hycP, similar to
//note="Rv0085, (MTCY251.03), len: 220. hycP, similar to
splP77524|HYFE_ECOLI HYDROGENASE-4 COMPONENT E (216
aa),FASTA scores: opt: 204 z-score: 272.1 E():1.2e-07;
25.5% identity in 216 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: In some cases we may not have predicted the currect initiation codon. Where possible we choose an initiation codon day, quy, or tupy which is preceded by an upstream ribosome binding site sequence (optimally 5-13pp before the initiation codon). It this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /qene-"hycD"
/note-"Rv0084, (MTCY251.02), len: 316,hycD, similar
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/strain="H37Rv"
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/organism-"Mycobacterium tuberculosis H37kv"
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/qene-"hycP"
967. .1629
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/gene="hycP"
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1 (bases 1 to 38380)
Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry Ill, C.E.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry Ill, C.E.,
Tekaia, F., Badcock, K., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.
Berrell, B.G.
Beciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT:006621"
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LLYELGLAGAPDVWITTLSKALGSQGGVVLGPTPVRAHLIDAARPFFFFFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAARAALRVI.OAEPWRPQAVI.NHAGĒLARMCGVAAVPDSAMVSV1 LGEPESAVAAAA
CLDAGVKVGCFRPPTVPAGTSRLRI.TARASLNAGĒLĒLARRVLTDVLAVARR"
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
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                                                                                                                                   /note="Rv1569, (MTCY336.34c), bioF, len: 386. Function: probable 8-amino-7-oxononancate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class.II pyridoxal-phosphate attachment site (PS00599). FASTA results, BIOF_MYCLE P45487(385 aa) opt: 1971; E(): 0; BO.1% identity in 381 aa overlap. Also similar to is mTCY10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in 393 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTCY251 38380 bp DNA BCr 03-AUG-2001
Mycobacterium tuberculosis H37Rv complete genome; segment 5/162.
274410 AL123456
274410.1 GI:3261600
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pyridoxal-phosphate attachment site"
6258. 6938
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Nature. 393 (6685), 537-544 (1998)
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6258. .6938
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                                                                                          5101. .6261
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                                  5101. .6261
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CDS

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/ John Rev 197. Unknown, some similarity to sp|P12999|BIOC_ECOLI BIOTIN SYNTHESIS PROTEIN BIOC. (251 aa). FASTA scores: opt: 202 z-score: 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
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98295987
2 (bases 1 to 43401)
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yqene="hyce"

yq
                                                                                            /yeural "nyc0066, (MTCY251.04), oxidoreductase, len: 488, /note="Ryc0066, (MTCY251.04), oxidoreductase, len: 488, hyco, most similar to splp74371HYFF_ECOLI HYDROGENASE-4 COMPONENT FEE 1. 656 dab, FASTA scores: opt: 948 z-score: 1117.4 E. (): 0: 35.9% identity in 493 aa overlap. Also similarto E. coli d9087711 & NUOL_ECOLI P33607 nadh dehydrogenaseichain 1 (613 aa) FASTA scores, opt: 360, deridap), and to NUON_ECOLI P33608, nadh dehydrogenase ichain n (425 aa), FASTAScores, opt: 375, z-score: 371.4, E(): 3.9e-14, (25.0% identity in 432 aa overlap) (codon_stati-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSVYKHAPSRVRLRQTRSTVVKGRSGSISWRRVRTGDIGLAVWG
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Ractional transferring Actinobacteria, Actinobacteridae;
Ractinal Firmientes Actinobacteria, Actinobacteridae;
Actinomycelales; Conyminateriniae; Mycobacteriaceue;
Actinomycelales; Conyminateriniae tuberculosis complex.

Mycobacterium; Mycobacterium tuberculosis complex.

E. (Charsel Let A 3401).

Raciole, S. T., Hrosch, K., Harkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S. V., Elglmeier, K., Gas, S., Barry III, C.E.,
Rarris, D., Gordon, S. V., Elglmeier, K., Gas, S., Barry III, C.E.,
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Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
L. Nature. 393 (6685), 537-544 (1998) tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.uk on Jun 27, 1998 this sequence version replaced gi:2104370. /transl\_table=11
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/db\_xref="di ö Mycobacterium tuberculosis H37Rv complete genome; segment 147/162. 295390 AL123456 Direct Submission Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium Gaps /Hote-"Rv0090, (MTCY251.08), len: 256. Unknown." 6147. .6152 /note-"aaggaq, potential rbs upstream of Rv0090" 6158. .6928 /qene="Rv0090" 6158. .6928 ; 0 91.1%; Score 16.4; DB 1; Length 38380; 94.4%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels 0; /product="hypothetical protein Rv0090"

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ALGARING MESPATTMIAUS CYRELIER FETALLECIOU CAATGALRARTTSI.
ALGALIA I VAAARA ALVALIER OSALGQAP I VMGRESGALIA UKUDOWHIVIINIASAR.
                                                                                                                                                                                                                                                               GAALAYAVDVKNAV LVAAAGNTGGAAQCPPQAPGVTRUSYTVAVSPANYDDY VLTVGS
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VSGLAAL LKARFPTLTARQVWQR LESTAHHPPAGWDPLVGNGTVDALAAVSSUS LPQA
GTATSDPAFVAVPVPRKSTPGPSDKRALHTAFAGAA LCLLALMATLATASKRLRPGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="RN3451, (WTCY13E12.04), len: 247. Function: probable cutinase, similar to several, contains cutinase, serine active site motif (FS00155). Alternative start possible at 373. FASTA results: CUT2_MYCTU 050664 probable cutinase cy339.08c precursor (219 aa) opt: 565; f): 2.3e-26; (44.88 identity in 223 aa overlap). Also similar to MYCY13E12.05 (FASTA score: E(): 0; (59.28 identity in 211 aa overlap).
                                                                                                                                                      PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGAGURVAVIDTGVA
RHRRLPRVVAGGDYVFTGDGTADCDAHGTLVAGIIAAAPDAQSDNFSGVAPDYIJISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mole-"PS00148 Serine proteases, subtilase lamily, serine octive site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"PS00137 serine proteases, subtilase family, histidine active site" 2456. 2488 /qune-"Rv3449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"PS00136 Serine proteases, subtilase family, aspartic acid active site"
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//dene="Rv3449, (MTCY13E12.02), len: 455. Function:
//note="Rv3449, (MTCY13E10 of series in the protection of signal properties of signal protection of series in the protection of signal pr
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ARMAVLLAGUSPRLPPALNPDDADALPTTDRLTTRANRADANLTSLLAAFAASAT (GA
1GTAVATHGIHRSSMGGIALAAVTGALLLLKAKSADTRRSLVFA (GGTTVATAFTVA
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WLCGAYSAVRHLDLTWT"
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GLAALLFAVTACRTYRDPIAGLTLSVIATI FGAVAGI,LAVPGVEGVIISVI,VAAMAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rv3448, (MTCY77.20), len: 467 aa. Unknown membrane protein, contains PS00402 Binding-protein-dependent transport systems inner membrane comp signature. Some similarity to AL021930 [MTV035_18 Mycobacterium tuberculosis (472 aa) fasta score, opt: 429 %-score: 488 4 E(): 1.1e-19; 28.2%identity in 479 aa overlap"
URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G 'C CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atq., grg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv3448"
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Submitted (10-MAY 2001) Takao Isogai, Helix Research Institute, Submitted (10-MAY 2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NUSDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) University of Tokyo.
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo
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precursor cells after 2-weeks retinoic acid (RA)
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/gene="Rv3452"
/note="Rv3452, (MTCY13E12.05), len: 226. Function:
probable cutinase precursor. Contains PS00155 Culinase,
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clone_lib:NT2RP3 clone:NT2RP3002701.
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Pred. No. 1.5e+02;
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Homo sapiens cDNA FLJ14743 fis, clone NT2RP3002701.
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Direct Submission
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/db_xref="G1:14042483"
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                                                            This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 other deletion regions (see AAT3355) and AAT3356) have also been detected identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of an avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see AAT33538-46), or by detecting the presence or absence of the sequences contained within heletion pollonarides are used as companients of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis DNA sequence encoding mammalian cell entry
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Detecting markers for avirulence in Mycobacterium – used in production of vaccines against bacterial infection, and to detect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0118442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US09863.
                                                                                                                                                                                                                                                                                                                             468 acatcaaagtgattcgcg 485
                                                                                                                                                                                                                                                                                                                    1 acatcaaagtgattcgcg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-115442/15.
                       bacterial infection
                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR71931.
                                                                                                                                                                                                           the deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                         09-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9506726-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rilev LW;
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ89200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                      AAQ89200
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A DNA molecule (AAT33656) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The encoded protein sequence is given in AAM02301. The DNA was obtd. by lighting M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cell-
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The Ah sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a serveted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                   Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellular uptake; cell entry; macrophage; passive immunisation; vaccine; gene therupy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                   Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product - macrophage survival protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                                                                                                                                                                                                                                      UB 16;
                                                                                                                                                                                                                                                                                                                                                                                                             ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= cell entry protein
886..1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis cellular uptake gene region.
                                                                                                                                                                                                                                                                                                                                                Score 16.4; UP
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 41; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT33656
ID AAT33656 standard; DNA; 1535 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/label= ORF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORK ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                      91.18;
94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0392210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*! ag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-425086/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW02301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riley LW;
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Gaps

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Indels

1;

Mismatches

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Conservative

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12-OCT-2001
                                                                                                                                                                                                                                                                02-AUG-2001
17;
                                                                                                            AAH99048;
                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                     Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
  Matches
                                                                                AAH99048
                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
 invasive clones. The DNA includes 2 separate coding regions (see also AAT38657-58) coding for the cell entry (AAW02302) and macrophage survival (AAW02303) proteins. It can be used to produce the cellular uptake proteins used as vaccines or to facilitate uptake of other
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                              .;
0
                                                                                          DB 17; Length 1535;
                                                                                                                                                                                                                                                                  DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                            Seguence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                              1;
                                                                                                                                                                                                                                                                                     Cellular uptake protein; vaccine; infection; ds
                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "stop codon not given"
                                                                                         Score 16.4; DE Pred. No. 12; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Pages 9-10; 82pp; English.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..1534
                                          materials, e.g. therapeutic genes.
                                                                                                                                                                                                       AAV18647 standard; DNA; 1535 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CONN-) CONNAUGHT LAB LTD. (CORR ) CORNELL RES FOUND INC.
                                                                                           91.18;
                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US13056
                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0689411
                                                                                                                                            1 acatcaaagtyattcgcg 18
                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                               (first entry)
                                                                                  Ouery Match
Best Local Similarity 94.*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-145620/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riley LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW47541
                                                                                                                                                                                                                                                                                                                                                                              W09805784-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-1996;
                                                                                                                                                                                                                                               03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Р,
                                                                                                                                                                                                                            AAV18647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chong
                                                                                                                                                                                               AAV18647
                                                                                                                                                                                     RESULT
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    888888
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Score 16.4; DB 19; Length 1535; Pred. No. 12;

91.1%; 94.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probbins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, maraque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cvw; fruit fly; yeast; hamster; macaque; horse; clonatc, monkey; dou; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2642 BP; 638 A; 703 C; 725 G; 576 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen R,
                                                                                                                                                                                                                                                                                         Human EST-derived coding sequence SEQ ID NO: 905.
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian XB, Wang
J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 723-724; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC76804 standard; cDNA; 2753 BP.
                                                                                                                                                         BP.
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A, Zhang J,
                                                                                                                                                       AAH99048 standard; cDNA; 2642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001WO-US02687
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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                     1 acateaaaqtgattegeg
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P-PSDB; AAM24389.
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Drmanac RA,
                                                                                                                                                                                                                                                 (Tirst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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AAC76804
1D AAC70
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100.0%;

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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; thrombolytic; communosuppressant; antimunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antilidabetic; hypotensive; dermatological; immunosuppressive; antilidabetic; hypotensive; dermatological; immunosuppressive; antilidabetic; antithyroid; and antibacterial; antiviral; antiliungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OKEX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, vectors.
                                                                                                                                                                                                                                                                                     Human, open reading frame, ORFX; detection; cytostatic; hepatolropic;
vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprolective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; intection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartiage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                  Human ORFX ORF2359 polynucleotide sequence SEQ ID NO:4717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2753 BP; 652 A; 746 C; 735 G; 619 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 3901-3903; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive; ss
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05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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P-PSDB; AAB42595.
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02-APR-1999;
                                                                                         08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiviral;
AAC76804;
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Length 2753;

DB 21;

88.9%; Score 16;

Query Match

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The present invention describes primer sets for synthesising 5602 [111]-length charks defined in the specification. Where a primer set comprises: (a) an oliqued primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence of an oligonucleotide comprises at least 15 nucleotides where the oligonucleotide comprises at selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length convas. The primers are also useful for the particularly without any specialised methods. And 1816 to AAMI18628 and AAMI3633 to AAMI3632 to AAMI3629 to AAMI3632 to AAMI3632 to AAMI3632 to AAMI3629 to AAMI3632 to AAMI3632 to AAMI3632 to a feature of the process the process and an amino acid sequences; and AAMI3629 to AAMI3632 to a feature of the process the process and an anino acid sequences; and an are used in the exemplification of the process the process and an anino acid sequences; and an account and account and anino acid sequences; and an account and account and account account and account account and account and account account and account account and account account anead in the exemplification.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                        Gaps
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                      Indels
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, Otsuki T;
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Wakamatsu A, Nagai K,
Pred. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence SEQ ID NO:17563.
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-01183767.
09-JUN-2000; 2000JP-02418997.
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                                                                                                                   453 catcaaaqtgatlege 468
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                          Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; immunestimulant; immunesuppressant; virucide; antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidabetic; antistumatic; antiinflammatory; dermatological; antidabetic; antistumatic; antiarthritic; antitheumatic; prologogide; antithyroid; immune deficiency; severe combined immunedeliciency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthmu; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia giuvis; insulin dependent diabetes mellitus; graft versus-host disease; autoimmune inflammatory eye disease; allergy; ss.
                                                                                                                                                                                                                                                                                                            Human secreted protein clone pt332_1 nucleotide sequence SEQ 1D NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating, preventing or ameliorating medical conditions in humans
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins-Racie LA, Evans C;
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                  Length 3125;
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              88.9%; Score 16; DB 22;
100.0%; Pred. No. 22;
ive 0; Mismatches 0;
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Agostino MJ,
                                                                                                                                                                                                         AAA16623 standard; cDNA; 3262 BP.
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98US-0099229
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                                                                                                        Best Local Similarity 100.
Matches 16; Conservative
                                                                                    2 catcaaagtyattcgc 17
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Clark HF, F
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04-SEP-1998;
23-OCT-1998;
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30-APR-1999
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                   Query Match
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                                                                                                                                                                              immunodelicienty (STID), as well as viral, bacterial, Inngal and other intections. These infections include human immunodeficiency virus (HIV), herpestineses, mycobacteria, Leismania spp., malaria and candidasis. The professes, mycobacteria, Leismania spp., malaria and as connective tissue disease, multiple sclerosis, systemic lupus crythomatosis, the una foid arthritis, autoimmune pulmonary inflammation, duillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetics mellitus, myasthenia quavis, graft-versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary uncleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis qenome with commercial importance. The products can be used to detect the presence
                                      which the protein is preferentially expressed, as molecular weight, markers on Southern gels, and as chromosome markers or trags to identity chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined
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animals. The polynucleotides can be used as markers for tissues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune inflammafory eye disease. The proteins can also be used to treat affergie conditions, such asthma. AAA16698 to AAA16774 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes for the human secreted proteins from the present invention.
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Pred. No. 22;
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100.08; Pro
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Best Local Similarity
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associated protein.
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                                                                                                                                                                                                                                                                                              Vaccine; prevention; treatment; infection; identification; binding compound; bacterfum; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
                      t
of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus taecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus!
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                Length 10594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos:544.546, aa:Xaa)
/transl_except= (pos:550..552, aa:Xaa)
/note= "Xaa = unknown; no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a Helicobacter pylori flagella
                                                                                      Sequence 10594 BP; 3197 A; 1733 C; 2323 G; 3337 T; 4 other;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                              aa:Xaa)
aa:Xaa)
                                                                                                                                                                                                                                                                              pylori flagella-associated protein ORF 19557055.aa.
                                                                                                                                                                                                                                                                                                                                                                                                       aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                  aa:Xaa)
                                                                                                                  20;
                                                                                                                                   1;
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                                                                                                                Score 15.4; DB Pred. No. 57;
                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            (pos:505..
                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= (pos:526./transl_except= (pos:535./
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 163-164; 1481pp; Enylish.
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                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/transl_except=
                                                                                                                                                                                                                         BP.
                                                                                                                  85.6%;
94.1%;
                                                                                                                                                                                                                         AAT67421 standard; DNA; 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US09122
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95US-0487032
                                                                                                                                                                  08-JUL-1997 (first entry)
                                                                                                                                                     1 acatcaaaqtgattcgc 17
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith D,
                                                                                                                                                                                                                                                                                                                                                                           633
                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052306/05.
                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASTR ) ASTRA AB.
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                                                                                                                                                                                                                                                                                                                              flagellum; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1996
                                                                    infection.
                                                                                                                                                                                                                                           AAT67421;
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                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                        RESULT
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homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypoptide production, e.g. in E. colf bosts.
The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori lite cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping conties generaled by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted cycling regions defined by computer evaluation. To identify likely H. pylori and idens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic, vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a H. pylori flagella-associated protein. The protein may be used in a vaccine to prevent or treat H. pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 639 BP; 222 A; 122 C; 132 G; 154 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DE
Pred. No. 82;
0; Mismatches
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88.9%;
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9508-0487032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*1.44
/male:
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASTR ) ASTRA
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useful as potential H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library; bacteria; human upper airway; otitis media: sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96109 BP; 28783 A; 18910 C; 20341 G; 28075 T; 0 other;
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                                                                                                                                                                                                                                                                                                          Length 1731;
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                                                                                                                                                                                                                                                    Sequence 1731 BP; 600 A; 302 C; 384 G; 445 T; 0 other;
                                                                                                                                                                                                                                                                                                            DB 18;
                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                  Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                              Score 14.8;
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                                                                                                                                                                                                                                                                                                            82.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                              422 acatcaaactcattcgcg 439
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic fragment #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-041427/05.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atheroselenosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thrombosmbolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atheroselerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarthy JJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensies, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "single nucleotide polymorphism"
   Length 96109;
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Score 14.8; DB 22;
Pred. No. 1.7e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene single nucleotide polymorphism #1697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary embolism; paternity test; ds.
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                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                             Db 14162 acatcaaaatgattctcg 14179
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      82.2%;
88.9%;
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2000US - 0225724
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                                                                                                                     1 acatcaaaqtqattcqcg 18
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      Query Match 82.2
Best Local Similarity 88.9
Matches 16; Conservative
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16-AUG-2000;
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                                                                                                                                                                                                                                                                                                   AAF96936
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Family 11 xylanase; improve; thermophilicity; alkalophilicity; thermocolerance; bleach; wood pulp; processing; wheat; maize; digestibilitiy-improving animal feed additive; starch production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified xylanase enzymes · useful for improving wood pulp
bleaching, etc.
                                                                                                                                                                                                                                                                                                                                                         DNA sequence of the specification.
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                                                                                                                                                                                                     AAV36098 standard; DNA; 573 BP.
                WPI; 1998-161100/15.
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                                                                                                                                                                                                                                                                                                          02-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                digestion and assimilation of nutrients. Xylanases the efficiency of digestion and assimilation of nutrients. Xylanases are preferred alignment added during the feed pelleting process. To survive the pelleting process and to have optimum activity in the animal, the ylandse needs to have high thermostability with optimum activity at physiological pul and temperature. Various xylanases have some properties suitable for feed applications but they lack the thermostability required to survive food pelleting. The present sequence is oligonucleotide, XyTv-104, from Trichoderma reesie. This sequence is oligonucleotide, XyTv-104, from Trichoderma reesie. This sequence was used along with 17 other overlapping oligonucleotides to construct the coding sequence for Trichoderma reesie xylanse Trx. The other oligonucleotides were:

XyTv-101 (AAA48229), XyTv-102 (AAA48230), Trx-103 (AAA48231), XyTv-2 (AAA48232), XyTv-110 (AAA48231), XyTv-2 (AAA48232), Trx-3 (AAA48232), Trx-3 (AAA48232), XyTv-110 (AAA48231), XyTv-5 (AAA48232), Trx-6 (AAA48232), Trx-6 (AAA48232), Trx-6 (AAA48232), Trx-109 (AAA48232), Trx-100 (AAA48232), Trx-100 (AAA48232), Trx-100 (AAA48232), Trx-100 (AAA48232), Trx-100 (AAA48232), Try-100 (AAA48232), Try-100 (AAA48232), Try-100 (AAA48232), Trx-6 (AAA48232), Trx-6 (AAA48232), Try-100 (A
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                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylanase; animal feed; digestion efficiency; thermostable;
feed pelleting; enzyme; XyTv-101, XyTv-102; TXT-103; XYTv-104;
XyTv-105; XyTv-106; XyTv-107; TTX-108; XyTv-109; XyTv-110; TTX-1;
XyTv-2; TTX-3; TTX-6; TTX-8; XyTv-4; XyTv-5; XyTv-7; Xyn A; Xyn B;
                        0;
                        Indels
                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                               T. reesei xylanase, XyTv-104, oligonucleotide.
Pred. No. 85;
); Mismatches
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                                                                                                                                                                                                                                                              AAA48232 standard; cDNA; 69 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xyn; Xyn C; Xyn I; Xyn II; ss.
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93.88;
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                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000 (first entry)
                        15; Conservative
                                                                                                                              1 catcaaagtgattggc 16
                                                                         2 catcaaagtgattcgc 17
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                  AAA48232;
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                                                                                                                                                                                                             RESULT
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Sung WL, Yaguchi M;

97EP-0115412. 9605-0709912

(first entry)

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0
                                                           The present sequence appears in the specification, which describes a method for modifying a Family II xylanase to improve its thermophilicity, alkalophilicity and or thermotolerance. This method comprises modification of amino acids 10, 27 or 29 of Trichoderma recess; xylanase
                                                                                                                                                                                                             If or corresponding displaced amono acids of another Family II xylanase, replacement of one of more amono acid sequences in the N-terminal region with corresponding aligned acqueres from another Pamily II xylanase to form a chimeric xylanase and/on upstream extension of the N-terminal by addition of upto 10 amino acids. The modified xylanses are useful for improving the bleechability of wood pulp by treatment at 55-75 degrees celsins and pH 7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-improving animal feed additives. They might also be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.4; DB 19; Length 573;
Pred. No. 1.4e+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the processing of wheat or maize for starch production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 573 HP; 163 A; 127 C; 136 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 2, 2002, 22:49:16 Job time: 9216 sec
Disclosure; Page 50; 84pp; English
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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Gaps

; 0

Length 69; Indels

80.0%; Score 14.4; DB 21; 93.8%; Pred. No. 1e+02; iive 0; Mismatches 1;

Conservative

Best Local Similarity Matches 15; Conserv

Query Match

Description		94 AR147694 Sequence 12. U35021 Mycobacteri 40 U45540 Mycobacteri 1. U35017 Mycobacteri					A96206 Sequence 23 88 U65788 Neisseria m 35 AF121135 Neisseria 94 AF313394 Neisseria		124769 Sequence 1 124769 Sequence 7 55 AP001255 Homo sapi 80 AC019980 Droscophil	AC019018 AC091965 AC008200	AC027490 AC008199	AE0037 6 AP0016 69 AB030	E06698 n 149752 S 163340 S	546012 polyprotein ALLGNMENTS	PAT 08-SEP-2000	008201.		ellular uptake of mycobacterium	tuberculosis and uses thereof Patent: US 6008201-A 5 28-DEC-1999; Location/Qualifiers 1650	94 t
DB ID		6 AR147694 1 MBU35021 1 MTU43540 1 MBDR3S1	1 AE0069 1 AF0418 6 186264 1 AE0070				6 A96206 1 NMU65788 1 AF121135 1 AF313394		5 124769 6 124769 9 AP001255 2 AC019980				ω	Š.	650 bp DNA	rom patent US 6 GI:10025753		)) ding for c	tuberculosis and uses thereof Patent: US 6008201-A 5 28-DEC-1999 Location/Qualifiers 1650	/organism≐"unknown" 258 c 185 g
ry ch Length	000	0000	.0 9764 .0 10019 .0 12412 .0 17783	000-			0.0.0.0	0.10.0.10.10	31010.0	.6 126253 .6 153865 .6 163687	10:0		3 742			2 ~		lassified. (bases 1 to 650) ey,L.W. molecule encodi	US 600820 Location,	/organisma a 258
Ouery Score Match		18 100.0 18 100.0 18 100.0	18 100. 18 100. 18 100.		2 8 8			115.4 85.6 115.4 85.6 115.4 85.6	9 99 90 10 10 10 10	5.4 85 5.4 85 5.4 85	88.57 7.58 7.58	5.4 85	m m m r 20 00 00 3	É		Sequence AR096715 AR096715.	Unknown. Unknown.	Unciassified. 1 (bases 1 t Riley,L.W. DNA molecule		123
Result No. S	351		8 9 c 10 11			19 20 21	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	34 35 36	37 38 39		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 AR096715/c LOCUS	DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL FEATURES SOUICE	BASE COUNT
GenCore version 4.5 Copyright (c) 1993 - 2000 Compusen Ltd.	using sw model	Run on: April 2, 2002, 22:46:04; Search time 2977.34 Seconds (without alignments) 99.736 Million cell updates/sec	Title: US-09-785-904-4 Perfect score: 18 Sequence: 1 catgccgtcgtattgctg 18	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1472140 seqs, 8248589755 residues  Total number of hits satisfying chosen parameters: 2944280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		4: gb_om:* 5: gb_ov:* 6: gb_pat:*	7: gb_ph:* {': gb_pl:* :: gb_pr:*	10: 9b_ro:* 11: 9b_sts:* 12: 9b_sts:*	13: gb_un:* 14: gb_uv:* 16: gb_vv:*		19: em_on: * 20: em_or: * 21: em_ov: * 22: em_pat. *		28: em_un:* 28: em_un:* 29: em_uh:*		34: em_htg_inv:* 35: em_htg_rod:* 36: em_htg_cther:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES

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Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K. Direct Submission
Submitted (29-AnG-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium bovis
Mycobacterium bovis
Actinobacteria: Actinobacteridae;
Actinomycelales; Corynebacterineae; Mycobacteriaceae;
Actinomycelales; Corynebacterium tuberculosis complex.
Mycobacterium; Mycobacterium tuberculosis complex.
Mycobacterium; Mycobacterium tuberculosis complex.
Mycobacterium; Mycobacterium tuberculosis of qenetic differences between Mycobacterium Molecular analysis of qenetic differences between Mycobacterium Movis actioniol 178 (5), 1274-1282 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="site of deletion breakpoint in this organism. virulent M. bovis has additional 10 kbp at this site" 637~\rm c 416~\rm g 214~\rm t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBU35021 1604 bp DNA BCT 27-APR-1996
Mycobacterium bovis BCG DNA flanking deletion region 3.
                           08-AUG-2001
                                                                                                                                                                Riley, L. W. and Chong, P.

UNA molecule fraqments encoding for cellular uptake of
Mycobacterium tuberculosis and uses thereof
Patent. 16224881-A 1 01-MAY-2001;
Location/Qualifiers
1. 1535
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                             PAT
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/sub_species-"BGG"
/db_xref="taxon:1765"
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 18; DB
100.0%; Pred. No. 40;
Live 0; Mismatches
                          AR147694 1535 bp DNA
Sequence 1 from patent US 6224881.
AR147694
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. 544 c 458 g
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                                                                                                                                      Unclassified.
1 (bases 1 to 1535)
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Matches 18; Conservative
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SOURCE
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VERSION
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TITLE
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AUTHORS
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Patent: US 6008201-A 1 28-DEC-1999;
Location/Qualifiers
1. 1535
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                               Score 18; DB 6; Length 650;
Pred. No. 47;
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Sequence 5 from patent US 6224881.
AR147696.1 GI:15111786
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Sequence 1 from patent US 6008201.
AR096713
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544 c 458 q
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258 c 185 g
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Riley, L.W. and Chong, P.
                                  100.0%;
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1 (bases 1 to 1535)
Riley, L.W.
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Matches 18; Conservative
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AR147696/c
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ADVEDAIRLVQGDITDAELVSQLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTF
                                                                                                                                                                                                                                                                                                                                                                                                   Rhamnose biosynthetic genes related to a novel repeated sequence of Mycobacterium tuberculosis
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Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
705-035, South Korea
3 (bases 1 to 3453)
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Daemyungdong, Namku, Taegu
                             Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds. 043540
                      14-AUG-1997
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                                                                                                                                                                                                                                                            Bacteria: Firmicutes, Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaccae; Mycobacterium; Mycobacterium tuberculosis complex.
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Submitted (14-AUG-1997) Tae-Yoon Lee,
Medicine, Yeungnam University, 317-1,
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Mycobacterium tuberculosis
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Actinomyrelates, Corynebacterineae; Mycobacteriaceae;
Mycobacterium, Mycobacterium tuberculosis complex.

1 (bases 1 to 9281)
Mahairas.G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium
bovis BCG and virulent M. bovis
J. Bacteriol. 178 (5), 1274 1282 (1996)
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Muhairas, 6.0., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K.
Direct Submitsation
Submitted (29-400-1995) Mark J. Hickey, Molecular Microbiology,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA
Location/Qualifiers
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/rinablaLion="MKGLHVVSKVTSAFFALFTPARRARKAAHVNLDQVAQCHKTDEG
/rinablaChtgartaged
/rinabl
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/hote-"similar to SP:P46840 P1D:559912; identified by
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                                                                                                                                                                                                                                          /note-"identified by Glimmer2; putative"
PPQTLHELRSHVRALLPGACIRRLLYGRVLVTWRAPV"
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                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein"
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/transl_table-11
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3791 ...4162
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/qene="MT0099.1"
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4206. .4973
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5105, 7390
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                                                                               /gene="MT0099"
3002. 3772
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ELDGSGTVRGNIKVPRAKLVVGSRSFSWRMI.FGLPVRTTSRVTALKPNH.LVECSHPLGH
RWRWEFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIFATLAKLSDO
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TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W. Whole genome comparison of Mycobacterium tuberculosis clinical and
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/note="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact; similar to SP:P16431 GB:X17506
PID:41684 PID:882614 GB:U00096; identified by sequence
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(bases 1 to 9764)

(bases 1 to 9764)

Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Relonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
                                                                                                        BCT 27-APR-2001 section 7 of 280 of the
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                                                                                                                                                               CDC1551,
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Mycobacterium tuberculosis CDC1551
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/note="clinical strain"
122. .1414
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Gill, J., Mikula, A. and Bishai, W.
Direct Submission
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1449. .2123
/gene="MT0096"
1449. .2123
                                                                                                                                                               Mycobacterium tuberculosis
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/gene="MT0098"
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/gene="MT0096"
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/gene="MT0098"
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Unpublished
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VERSION
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/transl_dable-11
/product_"putative 8-amino-7-oxononanoate synthase"
/prodein_d-"AAB96957.1"
/db.xref-"Gi:2791846"
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GLIFSSGYTANLGAVVGLSGPGSLLVSDARSHASLVDACRLSRAKVVYTPHRIVDAVD
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LLYELGLAGAPDVVMTTLISKALGSGÄGVVLGPPVRAHLIDAARPE FPDTGLAPAAV
GAARAALRVLAAEPWRPQAVLNHAGELARMCGVAAVPDSAMVSVTLAEPESAVAAAA
CLUAGVKVGGERPPTVPAGTSRLRLTARASLNAGELELARRVLTIVLAVAKK"
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/# H.LIRokogptrevitabisswapajibGHGHPALiQAL/TYQLYVBHGHPGGLTHPAAK
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VELVYG AAABELTHET VELGERDE RRYEVELLERDE FARGAFGAL GALFAADHAAVSP
FEBS VORALEGALSALAALE PADVAFESAGAAGALMIGDE FANREAT FANSVASVE
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VVFARGESQREVPESWarder SGPTRGTGTGTNTVGFDASGLLOYAYAGAGLKLPRSS
GONYRVGORVLPQQARKGDL PYGPEGTQSVALYLGKGQMLEV DVVOVSPVRTNGMT
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pngpedigpdagtesksaldepdektppritlriadwdvvctvvilavflavytmts
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LDGGWERPERILVYANIED TOTPAELTQTTSAMVEVARLAGSELC"
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PAASLKHRALTHTVPLAFSFERPASCEPLLSARSRRLVWVN"
                  Direct Submission
Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Mcdicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
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/product_"putalive
adenosylmethionine-B amino-7-oxononanoate
aminottansierase"
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/note-"BioP; similar to MRCY336,34c"
/codon_start l
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/hote="ORE2; similar to MYCY336.36"
/codon_start-1
                                                                                                                                                                                                                                                                      /hole-"ORF1; similar to MTCY336.37"
/codon_start l
                                                                                                                                               /organism "Mycobacterium bovis BCG"
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                                                                                                                                                                                                                                                                                                                         /transl_table 11
/product-"unknown"
/protein_id "AAB96954.1"
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/db_xret-"G1:2791844"
                                                                                                                                                                                                                           /db_xret-"laxon: 438'2"
                                                                                                                                                                                                                                                      complement (259, .1048)
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xret-"GL:2791844"
                                                                                              Location/Qualitiers
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/product-"unknown"
                                                                                                                                                                    /strain."Pasteur"
/sub_species "BCG"
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/qene "biok"
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Arene "bioA"
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/qene: "bioA"
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/qene-"biob"
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                                                                                                                                                    /product="hypothetical protein"
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/db_xref="G1:13879149"
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DGMDCBVAREALSSAEDGERAPVFSARVDEHLGEGCSACRAWFTQVASQAGDLRRLAES
                                                                                                                                                                                                                                                                           RPVVPPVGRLG FRRAPRROHSPMTWRKWALLCVGIAQIALGTVQGFGIJJVGLTHQHPT
GAGTHLLNESTSWSIALGVIMVGAALWPSAAAGLAGVLTAFVAILTGYVIVDALSGAV
STTRILTHLPVVIGAVLAIMVWRSASGPRPRPDAVAAFPDI VIJPDNASKGRRKGHLWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"conserved hypothetical protein"
/protein_id="AA.44326.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFEAVLAKLAAPGATNPDHHTPV TDTTPHAAATDRDTRSQAQRNHDGILAGGRALIAS
GKLGOHNGLPVSIVVTTTHTDLQTGAGKGFTGGGTLLPMADV FRNTSHAHHYSPASGR
YPQATFDHGTPLALYHTKRLASPAQKIMLFANDRGCTKPGGDAPAYHSQAHHVTAWTS
TGRTDTTELTLAGGPDNKLAEKGWTTHKNTHGHTEWLPPPHLDHGOPRVNTFHHPERF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by dolimmer2; putatives conserved hypothetical protein, authentic frameshift."

3103 c 3360 g 1748 L
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                                                                              /note="identified by Glimmer2; putative"
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/gene="MT0104"
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                             complement(7337. .8185)
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                                                        /gene="MT0102"
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RIFARPADFDTVGLSAGDHALTYYTQAPPVFRRRPLQIALTLMWPAGIASLVYALLA
AGTARDDLGGYPAVDPSSNARTEALETPQAFVS"
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1 (bases 1 to 12412)
Stover, C. Kendall and Mahairas, G.G.
Virulence-attenuating genetic deletions deleted from myrobacterium
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Mycobacterium tuberculosis CDC1551, section 114 of 280 of the
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteriac;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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Pred. No. 27;
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Pred. No. 28;
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                                                                                                                                                complement(9571. .>10019)
/note="ORFIL; similar to MTCY336.12"
/codon_start=3
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Matches 18; Conservative
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gene

CDS

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VEVPAELARGOTETLLSYQCATDAMSSRCFPSYALRRRAKALGSLTGMELLMESAALA
FEMAVSYPDHEGERGLAGSEY EPGYRVLDGTRAALNSERVGLSPATPTGLMGYSGGGL
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POPPRIASSAVEPPYLLI VQAVBDYLLI DVSD I DALADSYTAĞĞANVTYHRDI ESPHVSE
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Pett.son, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                         Flischmann, R.D., Miland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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/transl_table=11
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2997. .3236
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/gene="MT1624"
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Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
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1. .32437
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WAGVAYGDLEFIQFHPTMLFAGRAGGRRPLITEAIRGEGAILVSATTNPGSTGDGTALGE
WAGVAYGDLEFIQFHPTMLFAGRAGGRRPLITEAIRGEGAILVDRGGNS TTAGVHPMG
DARDVYAAAIDARLKATGDEVVLADAGSTGEGASRPPTVTYNSCRAAGIDPVRQP IP
VVPGAHYSCGGIVYNVGOFELLGIXAAGEVARTGLHGANRLASNSLLEGIVVAGRAG
KAAAARAAAGRSRATSSATWPEPISYTALDRGDLQRAMSRDASWYRAAAGLHRLCDS
LSGAQVRRDYACRRDFEDVALITVAQSVTAAALARTESRGCHHRAEYPCTVPEQARSIV
VRGADDANAVCVQALVAVC"
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Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3437)

1 (bases 1 to 3437)

1 (bases 1 to 3437)

2 (be.S.T. Brock,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,R., Gas,S., Barry 111,C.E.,
Harris,D., Gordon,S.V., Eiglmeier,R., Gas,S., Barry 111,C.E.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
squares,S., Sqares,J., Rutter,S., Zeeger,K., Skelton,S.,
squares,S., Sulston,J.E., Taylor,K., Whitehead,S. and
                                                                                                                                                           RGATVLAHNYOLPAIQDVADHYGDSLALSRVAAEAPEDTIVFCCVHFWAETAKILSPH
KTVI. IPDQRAGCSLADSITPDELRAWKDEHPCAVVVSYVNTTAAVKALTDICCTSSNA
VDVVASIDPDREVLFCPDQFLGAHVRRVTGRKNLHVWAGECHVHAGINGDELADQARA
HPDAELFVHPECGCATSALYLAGEGAFPAERYKILSTGGMLEAAHTTRARQVLVATEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="wagpawrdaadovvvIGTGvaGLaaaLaadraGksvvvLskaagT
HVTATHYAQGGIAVVLPDNDDSVDAHVADTLAAGAGLCDPDAVYSIVADGYRAVTDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGARLDESVPGRWALTREGGHSRRIVHAGGDATGAEVQRALQDAAGMLDIRTGHVA
                                                                                                                                        /translation="MTVLNRTDTLVDELTADITNTPLGYGGVDGDERWAAEIRRLAHL
                                                                                                                                                                                                                                                        GMLHQLRRAAPEVDFRAVNDRASCKYMKM1TPAALLRCLVEGADEVIIVDPG1AASGRR
    PID:1651334; identified by sequence similarity; putative"
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Pred. No. 26;
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                                                                         /product="quinolinate synthetase"
/protein_id="AAK45898.1"
/db_xref="GI:13881259"
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/protein_id="AAK45899.1"
/db_xref="GI:13881260"
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/trans1_table=11
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9021. .990R
                                                                                                                                                                                                                                                                                                                       /gene="MT1631"
7468. .9051
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/gene="MT1631"
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/gene="MT1632"
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Best Local Similarity 100.
Matches 18; Conservative
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IDGVKEFPGFWALVPVGATMLMILAGANROGHPGTRDRLPLDNRLLATAPI.VALGAMA YSWYLMHWPLLIFWLSYTGHRHANFVEGAAVLLVSGLLAYLTTRLVEDDFLYYRAPGVSRANSARAYDIPRRLERRPYT YLGSVYALGVALLATSFTWREINIVOKRAGKEL.SGLS RRDYPGARAI LIDVRYPKLLKRRPTVLEVRHDLPTSTREGGTSIFVNINAI INCTYGDVD APRTIALAGGSHAEHWLTALDLLGRMHHFKVVTYLKMGCPLSTEEVPI.IMGNNAPYPO
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LVVVLAGCALLT1AIOPOTRREAFANOSLASIGYYQNWELASTVSNYI.RAGEAVSPLQ
HIWSMSVQGOFYLAFLLLVAGCAYLLRRLFRGPRAPYLRTMFVVLLSTLTLASFIYAI
VAHHAYQATAYYNTFARAWELLAGALVGAVVPHVRWPWWLRTAVATAALAAII.SCGAL
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/translation="MLTLSPPRPPALTPEPALPPVTMGTRTTGFYRHDLDGLKGVAIA
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                                                                                                                                                                                                             Submitted (11-Jun-1998) Submitted on behalf of the Mycobacterium Liberchlosis Sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genelique Moleculaire Bacterienne, Institut pasteur, 28 rue du Dorteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:2117243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of M. Luberchlosis sequencing at the Sanger Centre are available on the World Wide Web.

(UKL, http://www.sanger.ac.uk/Projects/M_tuberchlosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observod/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct
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/strain-"H37Rv"
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/strain="H37Rv"
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/protein_id-"CARU9072.1"
/db_xref-"G1:2117272"
complete genome sequence
Nature. 393 (6685), 537-544 (1998)
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/clone-"Y48"
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LAKLLVDITPAGLDTVFFSDSGSVSVEVAAKMALQYWRGRGLPGKRRLMTWRGGYHGD
TFLAMSICDEHGGMHSLWTDVLAAQYRAPQVPRDPAYSAAREAQLAQHAGELAAVV
EVVVQGAGGMRFHDPRYTHDLRDICRYEVLLIFDEITGFGRTGALFAADHAGVSP
DIMCVGKALTGGYLSLAATLCTADVAHTISAGAAGALMHGPPFMANPLACAVSVASVE
LLLGQDWRTRITELAAGLTAGLDTARALPAVTDVRVCGAIGVIECDRPVDLAVATPAA
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                                                                                                                                                                                                                                                                          //note="Rv1566c, (MTCV336.37), len: 230. Function: unknown probably exported has QOAPV repeats at C.terminus, similar to hypothetical M. leprae protein, to putative invasins 1,2(007390, 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 procursor P60_LISMO P21171. FASTA results, Q49634 COSMID B1170 (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlap. TBparse scoreis 0.890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVTMTSWPSRLFAFTDNVCPPDACPLVPFGVNYY1YPVMWGGIG
CHOWYQAAMAKLVADHPDYVFTTSTRPWNIKPGDVMPATYVGIWQTFADNNIPVLAMR
DTPWLVKDGQPFIPADCLAKGGNPQSCGIARSKVLVDRNPTLDFVARFPLLKPLDMSD
AICRTDTCRAVEGNVLVYRDSHHLTPTYMRTMTSELGRQIAANTDWW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="possible RBS, AAGGAGG, for Rv1566c"
complement(3258. .3263)
/note="ASNI site: ATTAAT; probably linking fragments
B3/G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAIATAVIGPFVSMLKGWYMSFWPIISIAVITVTSIAGYAIAGFSEKYWH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDRGVWLRPFRNLVYAMPPYICTPAEITQITSAMVEVARLVGSLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein Rv1566c"
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/db_xref="G1:2117271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/protein_id="CAB09070.1"
/db_xref="G1:2117270"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:006624"
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/db_xref="G1:2117269"
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/gene="Rv1567c"
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                                                                                                                      complement(2327. .3019)
/gene="Rv1566c"
                                                                                                                                                                                                      complement(2327. .3019)
/gene="Rv1566c"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /qene="RV1567c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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AALKSRIDEQKAVVVTDSVFSADGSTAPVRELLEVCKRIGALTLIVDEAHGLÄVKÄGGRG
LLYFLGLAGADDVVMTPTLSKALGSQGGVVLGPTPVKAHLIDAARPFTPDYGLAPAAV
GAARAALKVLQAEPWRPQAVLNHAGELARMGGVAAVPDSAMVSVTIKEPESAVAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                    /Lrānslation-"MKAATQARIDDSPLAWLDAVQRQRHEAGLRRCLRPRPAVATELD
LASNDYLGLSRHPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQQFEABLAFFVGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            GLLFSSGYTANLGAVVGLSGPGSLLVSDARSHASLVDACRLSRARVVYTPHRDVDAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-11 pyridoxal-phosphate attachment site (PS00599). FASTA results, BIOF_WYCIE P$487(385 aa) opt. 1971; E(): 0; B0.18 identity in 381 aa overlap, Also similar to MTCY10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in 393 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis H7Rv complete genome; sequent 5/162.
                                                                                                                       Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLIDAGVKVGCFRPPTVPAGTSRLRLTARASLNAGELELARRVLTIVLAVAKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                   (MTCY336.34c), bioF, len: 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 32437;
/note="PS00600 Aminotransferases class-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ps00599 Aminotransferases class-II
pyridoxal-phosphate attachment site"
fqs8. .6938
6258. .6938
6258. .6938
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                   pyridoxal-phosphate attachment site"
5101. .6261
/qene="biof"
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                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SW1SS-PROT:006621"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 18;
100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                          /protein_id~"CAB09068.1"
/db_xref="G1:2117268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN2
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/transl_table=11
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                                                                                                                         /note="Rv1569,
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2 (bases 1 to 38380)
Parkhill,J.
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/gene-"bioF"
                                                                                                  /gene="biof"
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/yeue="nyco-
/note="Ry0008, (MTCY251.04), oxidoreductasc, len: 488,
hyco, most similar to splv77437|HYFF_ECOLI HYDROGENASE-4
COMPONENT F(EC 1.- (556 ad), FASTA scores: 0p1: 948
z-score: 1117.4 E(): 0; 35.98; identity in 493 ac overlap.
Also similarto E. coli dy08771 a NUOL_ECOLI P33607 nadh
dehydrogenasci chain 1 (613 aa) FASTA scores, opt: 560,
z-score: 354.9, E(): 4.2e-13, (27.98; identity in 488 ac
overlap, and to NUON_ECOLI P33608, nadh dehydrogenasci
chain n (425 aa), FASTAScores, opt: 375, z-score: 471.4,
E(): 3-9e-14, (25.0% identity in 432 ac overlap)"
//todon_start-1
//todon_te-"hyco"
//tb.cetin_id."CAA98922.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /worder myoungs, (MTCY251.05), oxidoreductase, len:
492, hyek, similar to HYCE_ECOLI P16631 formate
hydrogenlyase subunit 5 (569 aa) FASTA scores, opt: 680,
a x-score: H081, E(): 1.8e-38, (31.2% identity in 449 aa
overlap) and to NUOD_ECOLI P35600 nach dehydrogenase i
clain 6, (407 aa) FASTA scores, opt: 245, z-score: 293.1,
E(): 8,9e-10, (24.5% identity in 368aa overlap)"
/trodoc_Start-1
/troduct "hyee"
/product "hyee"
/product "hyee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:0108H5"
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/translation="MSVYKIIAPRRYRLRQPRSTSYSVEVAAPAR:1.FA1VADVRHHR
ELDGSGTVKGNIKWPKLVVGSKESTKWKLEGLPVRTTSRVTALKPRK-HI-04H
RWKWEFESLSPTLTRVTETPDYHAAGAIKNGLKFYEWTGFAKSNAAG1EATLAKL-SDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KESVAGETTVELKARIJAEVIHKGI EKIJEHGKPATAAVDI AEKI SÜDTSAAHALAHSLAI
EDALGI ELLEBUIRI IKALI VELERI, YHHADDIGALANIVOKSLANAHAÜK HENLIJAR
NAAVTGHELLEGA HAGGVALRALIPIYDELAALAVDI AEVATLI LANSVYYDEFAGTA
VILHPIDASALGGI GYVARASGI KSINAVEHPTIVLD TELGAHAGIIVI AKYT VEKNETE
AASAALAQH I VESHYGET EY AATLIIPVGAPSSGI GI VEGWEGT I VHKVELLIVDGKI TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAKLYGVLTEPAFLCAMVLAVTANN FGVTWA TEATTV I TAFLVGHRKTRTALEA FWKY
VV LCSVCTAVAFLGTVLLY FAARDSGAAAGALNED I LAEHAAGLDFGVARLAGGLLLL
LCYGAKAGLFPFHTWLADAHSQAPAFVSALMSGVCLLAVAFSVLTRLRFTLLAVSGPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7. 11. 105.1-01. 10.01. ""III. AAA., RHRY. ERGI, LATAFQI WADSI, KI ALVAAHDAGDSERV
VYLETA, VYTORRVELLA VVITADINI'EL KSLAYLSFFAGRFEREMADLYGI REVGHPRPR
REVRHAIMEPMILPMER FLAGTAPEFTETGAFPPLAVEGFYYETJEVGYVIAGLI EEGIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVIJAIG IGKTVIJELAGOJJOAAHDSTĀTAD TGVMRESKLĪGVSFAVGLIVIJĀJIJPP
AMFASFIJATAKSLANEKLAWVLGAALILITATGFTALAKNSCKNIJĀTPVAGATĀVPP
ATAAAAIMVGTVVSAALGTTAGPLADLIGTAASNVGLP"
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ampewmosoageoloolilkanalitvvmlvvtgivotataastoytneelalioth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIRNGELIVVGLATELIVAVEMETTTTVTGDVKRMLAYSSMEHMGETA LAAAAAGTTLA LAALEEL
MLDNGIAATAFLLTAGVPL[VELGASLDVLFAVIVIGVLTGKLRRIFGDADLDKLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MTCY251.06), len: 224. Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKVVDPSWFNWPALPVAMADT IVPDFPLANKSFNQSYAGNDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lransl_table-11
/product-"hypothetical protein Rv0088"
/protein_id-"CAA98924.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"sPFREMBL:Q10883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zab. xred. "Sa thribation con 0884."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zar xret "Grillov/E/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"G1:1405758"
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/note-"RV0088,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /qene-"kv0088"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3092. .4570
/qene="hyeE"
                                                                                                                                                                         /qene="hycu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3092. .4570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4605. .5279
                                                                      3095
                                                                                                          /qene≃"hycQ'
1629. .3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4605. .5279
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                                                                      1629.
                                                                             gene
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                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv0084, (MTCY251.02), len: 316,hych, similar to HYCD_ECOLI P16430 formate hydrogenlyase subunit 4 (307 aa) FASTA scores, opt: 570, z score: 591.6, E(): 2.1e-26, (33.8% identity in 305 aa overlap) and NUOLECOLI P33603nadh dehydrogenase i chain h (225 aa) FASTA scores, opt: 207, z score:220.7, E(): 9.5e-06, (26.5% identity in 260 aaoverlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLELĞTVALTLAGIDTGTSFGGMGASREITIAALVEPPILLAVFAL,SIPAGSANLGAL
VASTIDHPREHVVSLAĞVLARVEYNALIVI VIYAETGERLƏVDINASHHILBI "HWYHFAMYLEYAG
PRLALVEMAAGMRITYVALLALLANLFUPWGIAGAAPTALIOVLTGVVAVAAKVAILAVILA
ATFEVFLAKLRIFRVPELIAGSFLLALLANTAANFFTVGA"
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AAIPLLRGIRDNDRALIAVGLAVLALRALVLPWLLARAVGAEAAAQKEAFPLVNTASS
LLITAGLTLTAFAITQPVVNLEPGVTINAVPAAFAVVLLALFVMTTKLHAVSQAAGFL
                                                                         tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge Callo 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
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DLLKQLGKQQITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPIDPSADLFAVVG
                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidde. Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (itg, qtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                967. .1629
/gene="hycp"
/note="Rv0085, (MTCY251.03), len: 220. hycp, similar to
splP77524 |HYFE_ECOLI HYDROGENASE-4 COMPONENT E. (216
aa), FASTA SCOTES: OPT: 204 z-Score: 272.1 E():1.2e-07;
25.5% identity in 216 aa overlap"
       Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                        Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                  in Jun 27, 1998 this sequence version replaced gi:1405752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycobacterium tuberculosis H37Rv"
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/protein_id="CAA98920.1"
/db_xref="GI:1405754"
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/db_xref="GI:1405755"
                                                                                                                                                                                                                                                                                                                             available on the World Wide Web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="H37Rv"
/db_xref="taxon:83332"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hycP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="H37Rv
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6. of
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967. .1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="hycD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiation codon.
                                                                                                                                                                                                                                                       Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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       TITLE
JOURNAL
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probable precision of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 053863 SERINBFROTHSES (390 aa) opt: 241; E(): 8e-07; (38.0% identity in387 aa overlap), similar to MTCX15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAALDTTARPOO'QRTTELSGALAASC TAGGGLMLVRNALGTNVTRYSDATAGVVAAA
GLAALLEAV LA 'RETYRDELA'DTLESV LAT IFGAVAGLLAVPGVUGVIISVLVAAMAAAA
FSVLAMET GLG 'GGTTLTAVA' CTAVVYAAATUVGB TYAAPVE AGGSLATTASPGLLEVS
ARMAVILAGIG SPRLIPHODADALIPTURLTTRANKADAMITSLLAAFAST IGA
GTAVATHG IRKSSMOGLALAAVTGALLLARARSADVIRSLVEA IGG TTVATAPTVE
ADRALEHGPW I AALTAMLAAVAMFLGEVVAPALSLSPVTYRTIELLECLALIAMVPLTA
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GASPATAARYOLSALGAPALPMATTLAQCGTRDGAVLVLHKSSAQPPTPRCDDVAEAV
                                                                                                                                                                                                                                  of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct
                                                                                                          been renumbered from the original cosmid submissions but the old
deem designations are in brackets after the new gene numbers.
Gene prediction was based on a Hidden Markov Model of TB genes
implemented in TBparse (Krogh) supplemented with visual inspection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown membrane
                                                                                                                                                                                                                                                                                                                      initiation codon. Where possible we choose an initiation codon data, ada, or tudy which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream codon).
                  Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 z-score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport systems inner membrane comp signature. Some similarity to AL021930|MTV035_18 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis (472 aa) fasta score, opt: 429 z-score/484.4 E(): 1e-19; 28.2%identity in 479 aa overlap"/codon_start-1/1.ansl_table-11/product-"hypothetical protein Rv3448"/protein_in_archivel_in_cal_falle-1/db_xref="G1:3261767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, contains PS00402 Binding-protein-dependent
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/note-"PS00402 Binding-protein-dependent transport
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    43401
    /orqanism-"Mycobacterium tuberculosis H37kv"
    /strain-"H37kv"

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/strain="H37Rv"
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/clone="Y77"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLCGAYSAVRHLDLTWT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain-"H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1478. .2845
/gene="Rv3449"
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/gene="Rv3449"
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78. .164
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                                                                                                                                                                                                                                                                                                                                                                                                                     codon). If this initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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Actinomycetales; Corynebacterineae; Mycobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (Dases 1 to 43401)
Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry Ill,C.E.,
Takia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
Connor,R., Davies,R., Davlin,K., Feltwell,T., Gentles,S.,
Hamilin,N., Hollroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
NL Nature. 333 (6685), 537-544 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDQPWNANTHYDALLDAWVPLGTQCVLDVGCGDGLLAARLARRI
PYVTAVDIDAPVLRRAQTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANKVKGKWEHSAPIKWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                           /gene="Rv0089" (MTCY251.07), len: 197. unknown, some /note="Rv0089, (MTCY251.07), len: 197. unknown, some similarity to sp|P1299|BIOC_ECOLI BIOTIN SYNTHESIS PROPEIN BIOC. (251 aa). FASTA SCORES: Opt: 202 z-score: 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
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/note="aaggag, potential rbs upstream of Rv0090"
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Pred. No. 22;
; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:Q10886"
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/gene="Rv0090"
                            /gene="Rv0089"
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VNAQGEPSAFTLAGPWVDVAATGEAVTSLSPFGDGTVNRLGGQHGSIPISGTSYAAPV
VSGLAALIRARFPTLTARQVWQRIESTAHHPPAGWDPLVGNGTVDALAAVSSDSIPQA
GTATSDPAPVAVPVFRRSTPGPSDRRALHTAFAGAAICLLALMATLATASRRLRPGRN
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                                                                                                  /db_xref="G1:2104372"
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PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDOVWRLTRGAGGRVAVIDTCVA
                                                                                                                                                                                                                                                                                                                                                                                      RQSSSKFAPVGDPSSTGVGDVDTMAKAVRTAADLGASVINISSIACVPAAAAPDDRAL
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                                                                                                                                                                                                                                                                                                                                   RHRRLPKVVAGGDYVFTGDGTADCDAHGTLVAGIIAAAPDAQSDNFSGVAPDVTLISI
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complement (4049. .4081)

gene="Rv3450c"
/note="Rv3450c"
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/gene="Rv3450c"
complement(2810 .4222)
/gene="Rv3450c"
/note="Rv3450c" (MTCY13E12.03c), len: 470 Function:
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/gene="Rv3451"
/note="Rv3451, (MTCY13512.04), len: 247. Function:
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/note="possible RBS, GGAG,
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1862, 1894
/gene="Rv3449"
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4388. 5111
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/gene="Rv3449"
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TYGG. 473
/gene="Rv4451"
/note="PS00155 Cutinase, serine active site, GGYSGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssknA positive strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Mokhonov, V.V., Samokhvalov, E.I., Novikov, D.V., Shatalov, A.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 9600)
Mokhonov, V.V., Samokhvatov, E.I., Novikov, D.V., Shatalov, A.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"kv3452, (WTCY13E12.05), len: 226. Function:
probable cutinase precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (09-AUG-1999) Molecular Genetics, Ivanovsky Virology
Institute. Gamaleya Str., 6, Moscow 123098, Russia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF176573 9600 bp RNA VRL 18-AUG-199
Hepatitis C virus polyprolein precursor, gene, complete cds.
AF176573
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/note="isolated from acute hepatitis patient scrum"
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/note-"possible KBS, GAGG, for Rv3452"
5178. .5858
/qene-"Rv3452"
5178. .5858
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/protein_id="AAD50312.1"
/db_xref="GI:5738247"
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/strain-"274938U"
/isolate-"lb"
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/note="cleaved into C, El,
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Location/Qualitiers
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/qene="Rv3452"
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Hepatitis C virus
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Best Local Similarity
Matches 18; Conserv
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HSVWKDLLEDDFETPIDTTIMAKNEVFCVQPEKGGRRPARLIVFPDLGVRVCEKMALYD
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EESIYOCCDLAPEARCAINSLTERLYVGGPLTNSKGONGGYRRCRASGVLTTSCGWIL
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Gaps .; 91.1%; Score 16.4; DB 14; Length 9600; 94.4%; Pred. No. 2.1e+02; ive 0; Mismatches 1; Indels 0; Query Match 91.1 Best Local Similarity 94.4 Matches 17; Conservative

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Search completed: April 2, 2002, 22:46:14 Job time: 12544 sec

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Sequence 18, Appl
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24.647 Million cell updates/sec
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Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                   escription
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                                                      April 3, 2002, 08:04:13 ; Search time 165.4 Seconds
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                Compugen Ltd
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US-08-464-052-1
US-08-461-002-1
US-08-689-411-1
                                                                                                                                                           hits satisfying chosen parameters:
        GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                          351203 seqs, 113238999 residues
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Maximum Match 100%
Listing first 45 summaries
                                        OM nucleic - nucleic search, using sw model
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Sequence 15, April Sequence 29, Appl Sequence 5, Appl Sequence 7, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Seq
                                                                              Sequence 11, Appl
Patent No. 5248670
Sequence 15, Appl
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   Sequence Sequence 1
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APPLICANT: Stover, Charles K.
APPLICANT: Malairas, Gregory G.
TITLE OF SEQUENTIONS VIRULENCE-AFTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSER: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Stemant Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patenth Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/390.878 FILING DATE: 17 FEB 1995
                                                                           US-08-096-044C-9
US-08-149-105-1
US-08-317-847-1
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RESTERNATION NUMBER: 88,428
TOTAL SERVICE NUMBER: 154/1A 17
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PS: Compatible
OPERATING SYSTEM: PC-DOS/MS DOS
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10S-08-390-878-18
: Sequence 18, Application US/08390878
; Patent No. 5700083
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TRELEVAL: 415/54 1/2043
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12412 base pairs
TYPE: miclicic acid
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TELEPHONE: 415/541/9600
TELEFAX: 415/541/5043
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74.3 1238
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Best Local Similarity 100.
Matches 18; Conservative
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STATE: California
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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FILING DATE:
CLASSIFICATION: 536
                                         APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I'M FV COMPATIBLE
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08689411; Sequence 1, Application US/08689411; GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W. APPLICANT: Chong, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) US-08-689-411-1
                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-1
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NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1535 base pairs
                                                                                                                                                                                                                                                                      LENCTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                      nucleic acid
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CORRESPONDENCE ADDRESS:
                                                               FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rochester
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US-08-689-411-1
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Sequence 1. Application US/08461002
Patent No. 6214543
GENERAL INVORMATION:
GENERAL INVORMATION:
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                           Sequence 1, Application US/08464052
Sequence 1, Application US/08464052
Parent No. 6008201
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: GOLduman, Michael L.
REGISTRATION NUMBER: 30,727
REFERRNCE/POCKET NUMBER: 19603/185 (D-1485B)
TELEPHONE: (716) 263-F304
TELEPHONE: (716) 263-F304
TELEPAX: (716) 263-F304
TELEPAX: (715) 263-F305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT . PLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; D
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A.
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US-08-461-002-1
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                                                           RESULT 2
US-08-464-052-1
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TITLE OF INVENTION: CHALULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES TITLE OF INVENTION: CHALULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Hox 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.1%; Score 16.4; DB 4;
illarity 94.4%; Pred. No. 2.6;
Conservative 0; Mismatches 1;
ATTORNEY/AGENT INKORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/JOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1500
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION UNDRER: 30,727
REGISTRATION UNDRER: 30,727
RELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Gaps

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Indels

Length 4411529;

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DB 1; Length 573;
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APPLICANT: Yaqurili Dr., Makelo
APPLICANT: Yaqurili Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fitzpallic, Cella, Harper, and Scinto
STREET: 277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/U8/709,912
FILING DATE: 09. SEP 1996
CLASSIPITATION: 435
                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                           Score 16.4; DB pred. No. 7.8; 0; Mismatches
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Pred. No. 30;
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEGTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: _/desc - "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: O LSCH M., MALLOCH F.
KENTSHKAFFEH NUMBER: 27290
KEFFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICALION INFORMATION:
                                                                                                                   TYPE: DNA GORGANISM: Mycobacterium tuberculosis GORGANISM: Mycobacterium tuberculosis GOINER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08709912; Patent No. 5759840; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  DD 1789446 ACGTCAAAGTGAT"CGCG 1789429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ II NO: 18:
SEQUENCE CHARACTERISTICS:
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93.8%;
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94.48;
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.45
Matches 17; Couservalive
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US-08-709-912-18
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Best Local Similarity
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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US-08-709-912-18/c
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.6;
0; Mismatches 1; Indels 0
                                              Score 16.4; DB 4; Length 1535;
Pred. No. 2.6;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9409863
GENERAL INFORMATION:
APPLICANT: Piley, Lee W
TITLE OF INVANTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER PEDABALE FORM:
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19603/180 (D-1485)
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: GOLDMAN Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 30,727
RELEPHONN INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (716)263-1000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1535 base pairs
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MOLECULE TYPE: DNA (genomic)
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nilarity 94.4%;
Conservative
                                                    Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rochester
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US-09-103-840A-1/c
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PCT-US94-09863-1
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GENERAL INFORMATION:
APPLICANT: Cunningham Jr, Francis X
APPLICANT: DellaPenna, Dean
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-322-742-19
                                                                                                                                                                                                 LENGTH: 1959
                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                   APPLICANT: Stand Dr., Wing L
APPLICANT: Yaguchi Dr., Makkto
APPLICANT: Ishikawa Dr., Kazuhiko
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Firzbatric, Cella, Harper, and Scinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                           3: Fitzpatric, Cella, Harper, and Scinto 277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWART: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: -US/09/047,370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.4;
Pred. No. 30;
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /desc = "Synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09201641A; Patent No. 6232530
                                                                                                                                                             Sequence 18, Application US/09047370 Patent No. 5866408 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFRENCE/DOCKET NUMBER: 1039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2902
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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93.8%;
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 93.8
Matches 15; Conservative
                                                               471 CATTAAAGTGATTCGC 456
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           Conservative
                                            2 catcaaagtgattcgc 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CLONE: pTvX(3-190)
US-09-047-370-18
                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10172-0194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 277 Pa.
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                    US-09-047-370-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-201-641-1
           15;
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             Matches
                                                                                                                                  RESULT
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Gaps
TITLE OF INVENTION: Machod for Regulating Carotenoid Biosynthesis in TITLE OF INVENTION: Machod for Regulating Carotenoid Biosynthesis in FITLE OF INVENTION: Machod for Regulating Carotenoid Biosynthesis in FITLE OF INVENTION: Machod for NUMBER: US/09/201,641A CURRENT FILING DATO: 1998-11-30 NUMBER OF SEQ 1D NOS: 8 SOFTWARE: Patentin Ver. 2.0
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Pred. No. 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM FS/2 Model 50% or 558X OPERATING SYSTEM: IBM P.C. bus (Version 3.30) SOFTWARE WORLD-FEEL (Version 5.1) CURRENT APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: U.S.A.
Z.FP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
PRIOR APPLICATION DATA:
PROBLICATION NUMBER: 077918,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 077844,296
FILING DATE: February 28, 1992
FILING DATE: February 28, 1992
FILING DATE: February 28, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: February 28, 1992
APPLICATION UNMERK: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (304)..(1836)
; OTHER INFORMATION: beta-cyclase
US-09-201-641-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 14; Conservative
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DB 4;
            Score 13.8; DE
Pred. No. 81;
0; Mismatches
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93.3%; Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEDPLICATION NUMBER: US/OB/345,756
FILING DATE: 22-NOV-1994
CLASSIFCATION: 800
ATOONEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REPERNCE/DOCKFT NUMBER: 33229/236/1
TELEPHONE: (202)672-5309
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-625-198-6
; Sequence 6, Application US/08625198
; Patent No. 5756224
; GENERAL INFORMATION:
APPLICANT: Barbour, Eric
; APPLICANT: Hattori, Jiro
; APPLICANT: Hattori, Siro
; APPLICANT: Miki, Brian
                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08345756; Patent No. 5633438; GENERAL INFORMATION: APPLICANT: Bassrynski, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 MOLMOULE PYPE: DNA (spendule)
US-08-345-756-6
                                                                                                                                                               2059 catcaaattgattcacq 2075
                                                                                                                                 2 catcaaaqtqattcgcq 18
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 33 base pairs
TYPE: nucleic acid
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                                                                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Matches 14; Conserv
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20007-5109
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                                                                                                                                                                                                                                                                                                      US-08-345-756-6
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                                                                           Matches
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JEACHT NO. 812906

JEACHT NO. 812906

JETTLE DE INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MUDIFIED

JITLE OF INVENTION: FILAMENTOUS PHAGE

FILE REFERENCE: SCR2111S

CURRENT APPLICATION NUMBER: US/09/198,839

CURRENT FILING DATE: 1998-11-24

PRIOR PELING DATE: 1999-08-11

PRIOR PELING DATE: 1999-08-12

PRIOR PELING DATE: 1999-08-12

NUMBER: OF SEQ ID NOS: 11

SCOTUM NOS: 11

SCOTUM NOS: 11

SCOTUM NOS: 11

SCOTUM NOS: 11

CREATE: 2337

JENGTH: 2337

TYPE: DNA

TYPE: DNA

ATTER: DNA
                                                                                                                                                                     Gaps
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APPLICANT: Kang, Angray S.
TITLE OF INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MODIFIED
TITLE OF INVENTION: FILLAMENTOUS PHAGE
FILE REPRENENCE: SCR21115
FILE REPRENENCE: SCR21115
CURRENT APPLICATION NUMBER: US/09/198,839
CURRENT FILING DATE: 1998-12-24
PRIOR APPLICATION NUMBER: 60/096,326
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-11
SPRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: PORFES II US-09-198-839-2
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                                                                                                      DB 1; Length 358;
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                                                                                                                                                                     Indels
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                                                                                                         Score 13.8; DB
Pred. No. 61;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.8;
Pred. No. 81;
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US-09-198-839-3
; Sequence 3, Application US/09198839
; Patent No. 6190908
                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 2, Application US/09198839 Patent No. 6190908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.78;
                                                                                                            76.78;
88.28;
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                                                                                                                                                                                                                                                         262 CATCACAGTGATTCCCG 278
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                                                                                                                                          Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
; TOPOLOGY: linear
US-08-322-742-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 2321
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-198-839-2
                                                                                                                  Query Match
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0
Length 2337;
                                                                                                                                                                                                                                                                                   APPLICANT: Harbour, Eric
APPLICANT: Hattori, Jiro
APPLICANT: Hattori, Jiro
APPLICANT: Miki, Brian
TITLE OF INVENTION: MICROSPORE-SPECIFIC REGULATORY ELEMENT
WUMBER OF SHOUDENIES: 8
CORRESPONDENCE AND RESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM UC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Score 13.4; DB 5; Length 579;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCIT Text.
CURRENT APPLICATION DATA:
FPLING DATE: PCT/US96/05320A
FILING DATE: April22, 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 KEFERENCE/DOCKET NUMBER: 1488.014 PC01
TELECOMMUNICATION INFORMATION:
TELEBONE: (202) 371-2500
TELEFAX: (202) 371-250
TELEFAX: (202) 371-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 3, 2002, 08:07:11
Job time: 42191 sec
                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%;
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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446 TCAAACTGAFFAGGG 460
                                                                                                                                                                                                                                                                                                                             NAME: Eric K. Steffe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 tedaaqtqattegeg 18
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US96-05320A-1664
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APPLICANT: J. Craig Venter
TILE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome,
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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TITLE OF INVENTION: MICROSPORE-SPECIFIC REGULATORY ELEMENT WIMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                      COUNTY: USA

ZIP: 2000-5109

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,198
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/345,756
FILING DATE: 22-NOV-1994
ATTONNEY/AGERT IRPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; Pred. No. 72;
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PCT-US96-05320A-1664
; Sequence 1664, Application PC/TUS9605320A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences
; APPLICANT: 9410 Key West Avenue
, APPLICANT: Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltimore, MD 21205
United States of America
Mark D. Adams
Owen White
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Johns Hopkins University
720 Rutland Avenue
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TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERESTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%;
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Best Local Similarity 93.3
Matches 14; Conservative
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CITY: Washington
STATE: D.C.
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BG639721

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Database

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AQQ28124 RPC1-23-2
AL54224 0 AL543240
BF23803 601811750
AI513102 CH01393.3
BG718674 602659791
BF347054 60262879
AL520879 AL550879
AL559329 AL559329
AL559329 AL559329
AL556646 AL556646
BI115704 602866051
AL516794 AL54089
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3441.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA
5', mRNA sequence.
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BG382488 298399 MA
AW774157 EST333240
AQ091462 HS_3016_B
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AL525534 AL525534
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/Organism="Homo sapiens" //
/Organism="Homo sapiens" //
/Organism="Homo fetal heart, Lambda ZAP Express" //
/Clone_lib="Human fetal heart, Lambda ZAP Express" //
//Orde="Vector: Lambda ZAP Express; Site_l: EcoRI; Site_2: Xhol; mRNA was purified from human fetal hearts (8-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145)
Liew,C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Liew CC Contact: Liew CC Department of Laboratory Medicine and Pathobiology University of Toronto Banting Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel: 4169788758
                                                                        BF944889
BF927805
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BF490411
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AW390923
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PCR Pkimers
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
SC CCAGTCAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
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Unpublished (1997)
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BG639722
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 Fax: 4169785650
human.
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AUTHORS
TITLE
JOURNAL
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AA249381
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KEYWORDS
SOURCE
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BF351466 QV1-HT051
BF376314 CM0-TN003
BF376102 PM0-GN001
BF367003 PM0-GN001
D44620 HUMSUFPV017
BF77419 ILS-ITT002
AW750028 PM2-BT054
BF944885 CM1-NN019
AW248379 S220521.5
F05443 HSCOBH041 nn
F12193 HSC36H081 nn
                                                                                                       (without alignments) 50.427 Million cell updates/sec
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                                                                                         2002, 21:47:57 ; Search time 3835.7 Seconds
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Homo sapiens
Eukaryota; Mucracoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mucheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soarcs, F., Brentani, R.K., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&L2-CMO-TN0039-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF367020 375 bp mkNA EST 24-NOV-2000
MPG-CNV0118-130900-003-e09 GN0018 Homo sapiens CDNA, mRNA sequence-
BF367020
                                                                                                                                   BF376314 356 bp mRNA EST 24-NOV-2000 CM0-TN0039-2108U0-507-c05 TN0039 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sholgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 11; Length 356;
Pred. No. 4e+02;
0; Mismatches 0; Indels
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Seq primer: puc 18 forward
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High quality sequence stop: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%; Pro
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BF376314.1 CI:11338339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
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KEYWORDS
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(bases 1 to 160)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following UKI.
(http://www.ludwig.org.br/scripts/gethuml2.pl?t.j-QVIx12-QVI-HT0517-
020400-142-a088t3=2000-04-02xt4=1)
Seq primer: puc 18 forward.
Location/Oualifiers
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QVI-HT0517-020400-142-a08 HT0517 Homo saplens CDNA, mRNA sequence.
BF351466
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Suo Paulo-SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shorgun sequencing of the human transcriptome with \ensuremath{\mathsf{ORF}} expressed sequence tags
weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
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                                                                                                                                                                  Length 135;
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3.4e+02;
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                                                                                                                                                                ch 88.9%; Score 16; DB 1 Similarity 100.0%; Pred. No. 3.4 16; Conservative 0; Mismatches
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Fax: +55-11-2707001
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Best Local Similarity 100.
Matches 16; Conservative
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Contact: Shinji Hadano
Contact: Shinji Hadano
Japan Science and Technology Corporation, NeuroGenes Project, ICORP
Univ. of Tokai School of Med.
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-6095
Fax: 81-463-91-4993
                                                                                                                                                                                                                                                                   Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&12=PMO-GN0018-040900-002-008&43=2000-09-04&44=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 76.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Autonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcript map of the human chromosome 4p16.3 consisting of 627 cDNA clones derived from 1 Mb of the Huntington's disease locus DNA Res. 3 (4), 239-255 (1996) 97101646
                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIMSDIPY017 Human brain chNA Homo sapiens cDNA clone 003, mRNA sequence:
Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 4.1e+02;
0; Mismatches 0;
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1. .407
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/db_xref='taxon:9606"
/db_xref='taxon:9606"
/db_sref='taxon:9606"
/dev_stage="Adoult"
/dev_stage="Adoult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
/site_2: SmaI; A mini-library was made by choning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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1 (bases 1 to 407)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                         Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mosses 1 to 375)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F. F.,

Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-PMO&t2~PMO-GN0018-
130900-003-e09&t3=2000-09-13&t4=1)
Seq primer: pur 18 forward
High quality sequence stop: 375.
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Ludwig institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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              BF367020,1 GI:11329071
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Query Match 88.9
Best Local Similarity 100.
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1 (bases 1 to 427)

Dias Neto, E., Garcia, Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstehn, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_1: Smal; A min-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Fax: +55-11-2707001
Fax: +55-11-2707001
This satupson@ludwig.org.br
This sequence are can be seen in the following URL.
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-fl.5xt2-11.5-fr0027-121200-322-b06413-2000-12-12xt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                     BF772419 427 bp mRNA EST 12-JAN-2001
LS-TT0027-121200-322-b06 IT0027 Homo sapiens cDNA, mRNA sequence.
BF772419 GI:12120319
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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0. 4.1e+02; Indels
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                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="003"
/clone_lib="Human brain cDNA"
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113 c 120 g 71 t
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/clone_lib="170027"
/dev_stage="Adult"
                                                                                                             /tissue_type="brain"
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Adv. stage "Adull"

Adv. stage "Adull"

Anote—"Origin: breast; Vector: pucl8; Site_1: Smal; Site_2:

Smal; Anni-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

7716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue

mknA and cDNA amplification were performed under low
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AW750028
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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88.9%; Score 16; DB 11;
100.0%; Pred. No. 4.1e+02
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                  Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-270701
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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                      BF944885 166 bp mRNA EST 22-JAN-2001
CMI-NN0193-191000-484-g08 NN0193 Homo sapiens CDNA, mRNA sequence.
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2820521.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820521 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
/clone_lib="NN0193"
/dev_stage="Adult"
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Hong/Rubin Laboratory CNNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL) DNA Sequencing by: Berkeley MGC Sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lln.i.gov/Dbrp/Inage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/finage/fina
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Dovignes, M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
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1 (bases 1 to 238)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
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/organism="homo sapieus"
/organism="homo sapieus"
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/clone_lib="NHH_MCC_7"
/tissue_Lype="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 7.5e+02;
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                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 188.
Location/Qualifiers
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                                                                                                                                                      Unpublished (1999)
Other_ESTs: 2820521.3prime
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HSC0BH041 normalized inf
C-0bh04, mRNA sequence.
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94.18;
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/db_xref="taxon:9606"
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Matches 16; Conserv
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H14295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="togan: brain, vector: lafmid BA; Site_1: HindIII;
/site_2: NotI; sex=Female; dev_stage=3 months old;
/site_2: NotI; sex=Female; dev_stage=3 months old;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 301)

Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C., Devignes Auffray,C., Devignes, M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Poullot,Y., Sebastiani-Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
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HSC36H081 normalized infant brain cDNA Homo sapiens cDNA clone
c-36h08, mRNA sequence.
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Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-36h08
Seq primer: (-21)M13_universal.
Location/Qualifters
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             Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-0bh04
Seq primer: (-21)M13_universal.
Location/Qualifiers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_cree="taxon:9606"
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/clone=lib="normalized infant brain cDNA"
/sex="Female"
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Pred. No. 7.7e+02;
0; Mismatches 1;
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ilarity 94.1%;
Conservative
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F12193.1 GI:706535
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Fax: 33160778698
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Matches 16; Conserv
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/clone="c-36h08"
/clone="c-36h08"
/clone="th="normalized infant brain cDNA"
/sex="Female"
/tissue_rype="total brain"
/dev_stage="a months old"
/dev_stage="a months old"
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/note="Organ: brain; vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; vector: lafmid BA; Site_1: HindIII;
/note="organ: brain; vector bld;
/note="organ: brain; vector brain
/cloued 5' -> 3' Huto the HindIII -> NotI Sites of the
lafmid BA vector: Clone library from B.Soares, Psychiatry
/cloued 5' -> 3' Huto the Library from B.Soares, Psychiatry
/cloued 5' -> 3' Hoto the Library from B.Soares, Psychiatry
/cloued 5' -> 3' Inpersion_method:
/control process p. Na. S. in press"
/control process p. Na. S. in press.
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1 (bases 1 to 345)

1 (bases 1 to 345)

2 (billians)

3 (billians, M., Buthque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hullianson, A., Wohldmann, P. and Wilson, R., Willianson, A., Wohldmann, P. and Wilson, R. Ordrected: Wilson, R. Contact: Wilson R. Contact: Wilson R. Mashington University School of Medicine

4444 Forest Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: brain; vector: pT773D (Pharmacia) with a
modified polylinker; site_1: Not I; Site_2: Eco RI; lst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 114 286 1800
Fax: 144 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/clone="lmAGE:163571"
/clone=lib="Soares adult brain N2b4HB55Y"
/sex="Male"
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Pred. No. 7.9e+02;
0; Mismatches 1;
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Location/Qualifiers
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ilarity 94.1%;
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One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798

Fax: 510 486 6798

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Faxis shown the presence of a Khol site followed by a run of 14 or more Tresidues at the beginning of the sequence, this clone was polyadenylated. The resulting Polya" sequence has been removed. hit grounding Agoustians 1, 1444.2650,167635361

Figure SD.48 7004, 1017 484 7001

Figure SD.48 7004, 10 column: 10

Figure SD.48 7004, 10 column: 10

Figure SD.48 7004, 10 column: 10
      Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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//ordanism="brosophila melanogaster"
//do_aref="Leaxon:7227"
//clone="spo446"
//clone=lib="sp brosophila melanogaster Schneider 1.2 cell
culture porz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pOT2; Site_1: EcoR1; Site_2: Xhol; Sized fractionated cDNAs were directly ligated into pOT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.
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Eukaryota; Melazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryyota; Diptera; Brachycera;
Muscomorpha; Eblydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 380)
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Pred. No. 8.1e+02;
); Mismatches 1;
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Pred. No. 8.2e+02;
); Mismatches 1;
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Other_ESTs: SD04846.5prime
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BG639721.1 GT:13771230
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following UNL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1sL2=CM1-NN0193-301000-505-905st3=2000-10-30st4=1)
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/br xref="taxon:9606"
/db xref="haxon:9606"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal;
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        BF947972
        360 bp
        mRNA
        EST
        22-JAN-2001

        CM1-NN0193-301060-505-905 NN0193 Homo sapiens cDNA, mRNA sequence.

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with OkF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 8.1e+02;
); Mismatches 1; Indels 0;
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High quality sequence stop: 360
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Db 379 CATCAAAGAGATTCGCG 363

Search completed: April 2, 2002, 21:48:01 Job time: 10826 sec

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April 2, 2002, 22:49:16; Search time 366.19 Seconds (without alignments) 42.142 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	M. tuberculosis ma	DNA for M. tubercu	Mycobacterium tube	M. tuberculosis ce	DNA for M. tubercu	BCG deletion regio	Neisseria gonorrhe	Neisseria gonorrho	Neisseria gonorrhe	N. gonorrhoeae 1gt	Lipo-oligosacchari
	QI	AAT33658	AAV18649	AAQ89200	AAT33656	AAV18647	AAT33537	AAZ53670	AA212075	AA253673	AAT14061	AAT49230
	DB	17	19	16	17	19	17	21	20	21	17	18
æ	Query Match Length DB ID	650	650	1535	1535	1535	12412	1368	1779	1779	5859	5859
	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	85.6	85.6	85.6	85.6	85.6
	Score	18	18	18	18	18	18	15.4	15.4	15.4	15.4	15.4
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DMP53 tumour suppr C10-E15 DNA fragme C10-E12 DNA fragme Steptococcus pneu CFE 28 coding sequ 2CFE 28 coding sequ 2CFE 28 coding sequ 2CFE 28 coding sequ Streptococcus pneu Human colon cancer Hepatitis C virus Hepatitis C virus Hepatitis C virus Arabidopsis thalia Mouse neuropeptide DNA encoding human Non-A, non-B hepat 5'URY/CORE/ENV/NSI Human CYCCKINE alp BAC containing rep HCV envelope regio Aspergillus oryzae DNA encoding a hum phibacin PSBX orf Phibacin PSBX orf Phibacin PSBX orf Phibacin PSBX 1.2k TATA-binding prote Drosophila TATA-bi TATA-binding prote Ca mays DNA fragm Neisseria gonorrhe MEKK3 cDNA. Mus s Probe #17356 tor g Probe #17356 used Murine home morpho	ments  gene. ds. ATCC 25177).  to enter mammalian cells -
AAA53978 AAQ20926 AAQ20926 AAX20926 AAH90724 AAH90724 AAV2292 AAV2292 AAV2292 AAV2292 AAV2292 AAV2292 AAV22298 AAV222398 AAV222238	ALIGNM ALIGNM jival g cropha acropha hin H37 hin H37 filty tc ge(S),
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11111111111111111111111111111111111111	RESULT AAT33658, XX XX AAC AAT DT 22-1 DE W XXX XX X
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tuberculosis, to induce a passive immunity and prevent disease
                                 Sequence 650 BP; 123 A; 258 C; 185 G;
                                                                                                                                                                                                                                                                                                  Vaccine; tuberculosis;
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                                                                             Best Local Similarity
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             occurrence
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                A DNA molecule (AAT33658) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT33656) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. colistrains for Hela cellinvasive clones. It can be incorporated into a vector and used for prodn. Of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule (tuberculosis the ability to enter mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antihiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to
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                                                                                                                                                                                          100.0%; Score 18; DB 17; Length 650; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis cellular uptake protein fragment.
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                                                                                                                                                          Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
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/note= "stop codon not given"
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Claim 7; Page 45; 67pp; English
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          DNA for M.
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                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a secreted protein, a cytophasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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                                                                Length 650;
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84 T; 0 other;
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                                                                   DB 19;
                                                                Score 18; DB
Pred. No. 1.9;
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100.0%; Pred. No. 2;
ive 0; Mismatches
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                                                              100.0%; Some 100.0%; Protive 0;
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Best Lucal Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                                           189 CATGCCGTCGTATTGCTG 172
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22-NOV-1996

AAT33656;

AAT33656/c

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Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic ayents e.g. antibiotics, also useful in vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
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                                                                                                                      DNA for M. tuberculosis cellular uptake protein fragment.
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                                                                                                                                                          Cellular uptake protein; vaccine; infection; ds
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/note- "stop codon not given"
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Mismatches
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100.0%; Pred. No.
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ID AAV18647 standard; DNA; 1535 BP.
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                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                     03-JUL-1998 (first entry)
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                    Cellular uptake; cell entry; macrophage; passive immunisation; vaccine; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= macrophage survival protein
                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
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100.0%; Pred. No. 2;
ive 0; Mismatches 0;
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886..1535
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/label= ORF-1
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/label= ORF-2
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       1074 CATGCCGTCGTATTGCTG 1057
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                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                      181..810
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P-PSDB; AAW02301

Riley LW;

WO9626275-A1

Key

CDS

29-AUG-1996.

20-FEB-1996; 22-FEB-1995;

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Gaps

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Indels

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RESULT

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W09924578-A2
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                                30-APR-1999;
                                                                                                                                                                                                        Petersen J,
Tettelin H,
                                                                   31-JUL-1998;
02-SEP-1998;
                                                                                       02-SEP-1998;
09-OCT-1998;
                                                                                                               09-0CT-1998;
                                                                                                                                      25-FEH-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999.
          11-NOV-1999
                                                                                                                          09-OCT-1998
                                                                                                                                                                                              Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ12075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
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                                                                                                                                                                                                                                                                                                                  This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region casults in an avirolence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33536) have also been detected. Identification involved Screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of a virulent, or a virulent, mycobacterial phenotype. Determination of a virulence requires the detection of the presence or absence of presence or absence of absence of absence of absence of the sequences contained within the deletion. Deletion junctions (see AAT33538-46), or by detecting the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saps
                                                                                                                                                                                                                                                     Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria gonorrheae ORF 311 partial DNA sequence SEQ ID NO:1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 17; Length 12412; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                       /*tag= a
/note= "BCG delta 1 deletion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                Location/Qualifiers
1406..10673
                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA253670 standard; DNA; 1368 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
          Mycobacterium bovis strain BCG
                                                                                                                                      96WO-US01938
                                                                                                                                                            95US-0390878
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                                                                                                                                                                                   (PATH-) PATHOGENESIS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                          Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrheae.
                                                                                                                                                                                                                               WPI; 1996-393419/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                          Mahairas GG,
                                 Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09957280-A2
                                                                                                                                     15-FEB-1996;
                                                                                                                                                             17-FEB-1995;
                                                                                          WO9625519-A1
                                                                                                                 22-AUG-1996
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AAE53015 to AAE54536, AAE54577 to AAE54615, and AAY74253 to AAY75941 represent nevel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAE54571 to AAE54576 and AAE54616 to AAE5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for trealing or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antiagonists, which may themselves have use as antibodieterial agent S. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1368 BP; 287 A; 377 C; 448 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>:</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Galeotti C, Grandi G, Hickey E,
, Pizza M, Rappuoli k, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.6%; Score 15.4; E
94.1%; Pred. NO. 49;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 709; 1453pp; English.
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                                                                                       98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
                                                                                                                                                                                                                  98US-0103794.
98US-0103796.
99US-0121528.
99WO-US09346.
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                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae.
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P-PSDB; AAY74908.
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Bost Local Similarity
Matches 16; Conserv.
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, Mora M; Scarselli M;

Masignani V, Scalato E, S

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represent novel Neisseria meninglis and N. gonorrheae polynucleoides and polypeptides. AAX54537 to AAX54576 and AAZ54616 to AAZ55473 represent polypeptides. AAX54537 to AAX54576 and AAZ54616 to AAZ55473 represent polypeptides, unbedieved to the present invention. The polypeptides, the polynucleoides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to be isserial bacteria (e.g. meningits and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antiagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA253015 to AA254546, AA254577 to AA254615, and AAY4253 to AAY75941
                                                                                                                                                                                                                                                                                                               Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosyltransterase; lipo-oligosaccharide; 1gt gene; LOS locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1779 HP; 367 A; 478 C; 599 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 712-713; 1453pp; English.
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/note= "poly-G tract"
1491..2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Localion/Qualifiers
                                                                                                                                                         Rappuoli R,
                                                                                                                                Caleotti C, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae strain F62.
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/product= LgtA
699..715
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/product= LgtC
2499..2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.6%;
Best Local Similarity 94.1%;
Matches 16; Conservative
99US-0121528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 atgregtestattsetg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 1491
                                                                                                                                                                                                                                                                                                                                              vaccines and diagnostics
                                                                              (GENO-) INST GENOMIC RES
                                                                                                                                                            Pizza M,
Vente: JC;
                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                       WPI; 2000-062150/05.
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                                                                                                                                                                                                                                                                   P-PSDB; AAY74911.
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                                                                                                                                Fraser C, Ga
Petersen J,
Tettelin H,
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT14061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAN A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequences AA211972-212358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins from Neisseria meningitidis and N. gonorrhoeae uscful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrheae ORF 311 partial DNA sequence SEQ 1D NO:1295.
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                                                                                                                                                                                                                                                                                                                                                    Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                    Grandi G, Masignani V, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.4; D
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 175; 524pp; English.
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980S-0098094.
980S-0099062.
980S-0103749.
98US-0103794.
                                                                                98GB-0019016.
97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0025147.
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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                                    98WO-IB01665
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                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-327407/27.
                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY38618
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9957280-A2
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                                 09-OCT-1998;
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                                                                                                                                                                                                                                                  14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1999
                                                                                         01-SEP-1998
                                                                                                                                        14-NOV-1997
                                                                                                                                                                    18-NOV-1997
27-NOV-1997
                                                                                                                                                                                                                   10-DEC-1997
                                                                                                                  06-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ53673;
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AA253673 RESULT

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Gaps

0;

Indels

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Length 1779;

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poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both Glenac and Galnac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW06576, AAW06577, AAW06578, AAW06580.
                           /product= polyglycosyltransfarase
                                                                                                                                                                                                                                                                                                                                                                Transfer of at least 2 saccharide units using
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2A-H; 38pp; English.
                                                                                                                                                                                                                                                                                            Johnson KF, Roth S;
                                                                                                                                                                                                                                                               (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                   95US-0478140.
                                                                                                                                                                                                       96W0-US08323
                                                         /*tag= c
3322..4335
/*tag= d
4354..5196
/*tag= e
                                         2342..3262
               /*tag= b
445..1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                             single galactose molety
                                                                                                                                                                                                                                                                                                                        WPI; 1997-052451/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Lical Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200055178-A1.
                                                                                                                                               WO9640971-A1
                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000
                                                                                                                                                                           19-DEC-1996
                                                                                                                                                                                                                                                                                            Buczala SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA53978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                       CDS
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 CDS
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The lgt locus (AAT14061) of Neiserria gonorrhoeae F62 contains 5 open reading frames, 1gth, 1gtb, 1gtC, 1gtD and 1gtE, coding for 5 glycosyltransferases (see also AAR9131-15) involved in gonococcal lipooligosaccharide (LOS) biosynthesis. The sequence was constructed from 2 clones isolated from an F62 gene bank in lambda-200 following screening with plasmid pR10p1. 3 of the coding sequences contain poly-G tracts that make them susceptible to premature termination. The lgt coding sequences can be used for prodn. of recombinant LGT glycosyltransferases that are utilised in biosynthesis of LOS useful in vaccine prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Neisseria and for the biosynthesis of oligo:saccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipo-oligosaccharide (including polyglycosyltransferase) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5859 BP; 1411 A; 1462 C; 1661 G; 1325 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR91311, AAR91312, AAR91313, AAR91314, AAR91315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.6%; Score 15.4; DB 17;
94.1%; Preu. No. 54;
live 0; Mismatches 1;
 /note= "poly-G tract"
3322..4335
                                                                        /*tag= g
/note= "poly-G tract"
4354..5196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria gonorrhoeae ATCC 33084.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2g-m; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT49230 standard; DNA; 5859 BP.
                              /*tag= f
/product= LgtD
3576..3586
                                                                                                                                 /product = LgtE
                                                                                                                                                                                                                        95WO-US12317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.6
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER.
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/*tag=
                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                       WPI; 1996-200924/20.
                                                                                                                                                                                                                                                                                                             Gotschlich EC;
                                                             misc_feature
                                                                                                                                                               WO9610086-A1
                                                                                                                                                                                                                                                     26-SEP-1994;
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                                                                                                                                                                                            04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT49230;
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                 CDS
                                                                                                      CDS
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Gaps
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A lippoligosaccharide-encoding gene region (AAT49230) of Neisseria gonorrhoeae ATCC 33084 includes a coding sequence for a novel Neptylytycosyltransferase (PGTase) (AAM065576) that catalyses the addition of both GirNac and GalNac disaccharides to a single galactose molety. The products (AAW06577-80) of the other coding sequences of this region are not identified. The PGTase gene can be obtd. using standard techniques and incorporated into a vector to allow produ. of the PGTase in transformed host cells. The enzyme is useful in the synthesis of oligosaccharides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5859;
                                                                                                                                                                                                                                                                                                                                             Sequence 5859 BP; 1407 A; 1462 C; 1661 G; 1329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.4; 19 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA53978 standard; DNA; 27425
                                                                                                                                                                                                                                                                                                                                                                                                                                             85.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.18;
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09-JUL-1990;
30-NOV-1990;
              20-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1990;
30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ20923;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                             Maki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maki N,
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ20923/c
ID AAQ20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                     metazoan invertebrate organisms, such as insects and worms, or cultured corls, resulting in p53 expression or mis-expression. The cultured cells, resulting in p53 expression or mis-expression. The tumour su pressor genes, a p53 polypeptide or genetically modified organisms or cells are used in screening assays to identify compounds or molecules, preferably a pharmaceutical agent or a pesticide, that modilates p53 activity. The genetically modified organisms or cells are also useful for studying p53 activity by detecting the phenotype caused by the expression or mis-expression of the p53 protein in the insect. The method additionally comprises observing a second insect having the same genetic modilication as the previous one, which causes the expression or mis-expression of the p53 protein, where the second animal additionally comprises a mutation in a desired gene and differences between the-pfenotype of the first and second identifies the desired gene as capable of modilying the function of the gene encoding the p53 protein. The genetically modified organisms or cells are also useful for identifying other genes modulating the
                                                                                                                                                                          Novel p53 tumor suppressor gene encoding a protein useful for genetically modifying metazoan invertebrate organisms, such as insects for screening compounds of pharmaceutical use or a pesticide
                                                                                                          Keegan KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C10-E15 DNA fragment encoding NANBH-specific antigen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 27425;
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0
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                                                                                                          Ollman MM, Young LM, Demsky MR,
C, Larson JS, Robertson SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-A non-B hepatitis virus; recombinant; detection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DE
Pred. No. 60;
0; Mismatches
                                                                                                                                                                                                                                 Example 7; Page 80-89; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.6%;
Best Local Similarity 94.1%;
Matches 16; Conservative
          13-MAR-2000; 2000WO-US06602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ20926 standard; DNA; 742
                                      99US-0268969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-A non-B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91EP-0306158
                                                  23-FEB-2000; 2000US-0184373
                                                                                                          Platt DM, Oll
Kopczynski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9553 AGGCCGTCGTATTGCTG 9537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                              (EXEL-) EXELIXIS INC.
                                                                                                                                                  WPI; 2000-638178/61.
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                                      16-MAR-1999;
                                                                                                          Buchman AR,
Friedman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ20926/c
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The sequence is that of a DNA fragment encoding a non-A non-B (NANB) hepatitis-specific antigen polypeptide, it can be used to produce the polypeptide recombinantly. It is derived from the DNA clone C10-F15. It can be used to dive PCP primers which are capable of detecting NANB hepatitis with high accuracy. See also AAQ20617-Q20629 and
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-A, non-B hepatitis-specific antigen polypeptide - for detection of hepatitis virus gene or antibody directed against virus

    for detection

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C10-E12 DNA fragment encoding NANBH-specific antigen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                      Length 742;
                                                                                                                                                             Non-A, non-B hepatitis-specific antigen polypeptide - for of hepatitis virus gene or antibody directed against virus
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-A non-B hepatitis virus; recombinant; detection; ss.
                                                                                                                                                                                                                                                                                                                                           Sequence 742 BP; 129 A; 217 C; 209 G; 187 T; 0 other;
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0
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77;
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                                                                                        Kohara M;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Score 15;
Pred. No.
                                                                                        Toyoshima A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toyoshima A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local ion/Qualitiers
                                                                                                                                                                                                          Claim 18; Fig 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                       83.3%; (
90JP-0413844.
90JP-0180889.
90JP-0339589.
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90JP-0180889.
90JP-0339589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-A non-B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 catgccgtcgtattg 15
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                                                                                        Yamaguchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamaguchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 CATGCCGTCGTATTG
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                                                                                                                    WPI; 1992-034390/05.
                                                         (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR20720
                                                                                                                                   P-PSDB; AAR20723
                                                                                                                                                                                                                                                                                                                AAQ20922-Q20925.
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The present sequence encodes the Streptococcus pneumoniae filty-four homologue (ffh) protein, which is a component of the protein secretory apparatus in bacteria, and the bacterial homologue of the eukaryotic Signal Recognition Particle. Fith proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of Ffh protein by identifying mutations in the Ffh gene, or determining Ffh protein or mRNN expression levels due to an infection of an organism with the Ffh gene. They can diagnose the stage and type of infection. Ffh proteins are also useful for screening for compounds which affect activity of the protein by measuring the binding to ffh protein and observing the stimulation or inhibition of the protein function. These can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance (agonist) Ffh activity, in addition to direct administration of Ffh
                                     The sequence is that of a DNA fragment encoding a non-A non-B (NANB) hepatitis-specific antigen polypeptide, it can be used to produce the polypeptide recombinantly. It is derived from the DNA clone C10-E12. It can be used to give PCR primers which are capable of detecting NANB hepatitis with high accuracy. See also AAQ20617-Q20629 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus pneumoniae Fifty-Four Homologue (Ffh) polypeptide and polynuclectide - useful as diagnostic reagents and for prevention and treatment of Streptococci infections, which cause otitis media, sinusitis and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; "ffh; fifty-four homologue; antibacterial; infection; otitis media; conjunctivitis; bacteraemia; sinusitis; pleural empyema; endocarditis; meningitis; ds.
                                                                                                                                                                                                                            Length 932;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                   Sequence 932 BP; 173 A; 276 C; 257 G; 226 T; 0 other;
                                                                                                                                                                                                                            DB 13;
78;
                                                                                                                                                                                                                          83.3%; Score 15; DB 100.0%; Pred. No. 78; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae ffh encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 5-6; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX19484 standard; DNA; 1569 BP.
           Claim 15; Fig 15; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          970S-0923772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
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Best Local Similarity 100.
Matches 15; Conservative
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direct administration of antisense sequences to prevent expression. Ffh proteins (administration of antisense sequences to prevent expression. Ffh proteins (administered directly, in a vector and as a vaccine) and antibodies induce an immune response to immunise and prevent disease. Diseases diagnosed, prevented or treated include: bacterial infections, especially Streptococcus pneumoniae infections, which cause otitis media, conjunctivitis, bacteraemia, sinustias, pleural empyema, endocarditis and especially meningitis. Ffh proteins, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
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Pred. No.
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100.0%;
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TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
CITY: New York
                                    sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 1, Appli
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Pred. No. 0.81;
); Mismatches 0; Indels
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NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REGISTRATION NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                    US-08-248-839C-5
US-08-248-839C-1
US-08-248-839C-7
US-08-646-715-1
US-08-646-715-1
US-08-35-670B-10
US-08-33-576C-12
US-08-333-576C-12
US-08-808-324-10
US-08-808-324-10
                                                                                                                                                                                                                                                                            PCT-US94-14030A-10
PCT-US94-14030A-12
US-08-362-670B-1
PCT-US95-10398-18
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                              US-08-333-576C-1
US-08-808-324-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08464052; Patent No. 6008201; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
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Best Local Similarity 100.
Matches 18; Conservative
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STRANDEDNESS: double
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CLASSIFICATION: 435
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Sequence 5, Appli
Sequence 1, Appli
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/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seg:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seg:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-461-002-5

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US-08-464-052-1

US-08-461-002-1

US-08-461-002-1

US-08-461-002-1

US-08-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-09-103-840A-1

US-08-312-387B-1

US-08-312-387B-1

US-08-683-426-7

US-08-683-426-7

US-08-683-458-7

US-08-478-140B-1

US-08-478-140B-1

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US-08-449-093A-18
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Maximum Match 100%
Listing first 45 summaries
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Title: Perfect score:

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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-464-052-1
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                                       FILING DATE:
CLASSIFICATION: 536
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US-08-464-052-1/c
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                                                                            APPLICANT: Riley M.D., Lee W.
TILE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DAPPLICATION NUMBER: US/08/461,002
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US-08-689-411-5/C

US-08-689-411-5/C

US-08-689-411-5/C

Sequence 5, Application US/08689411

Patent No. 6224881

GENERAL INFORMATION:

APPLICANT: Riley M.D., Lee W.

APPLICANT: Chong, Pele

TITLE OF INVENTION: CELLULAR UPTAKE OF WICOBACTERIUM TUBERCULOSIS AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNAY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERCECCET NUMBER: 30,727
RELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-14600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                 Sequence 5, Application US/08461002 Patent No. 6214543 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-5
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A.
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AFFLICANT: RILEY M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon. Harresseen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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NAME: Goldman, Michael L.
REGISTATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREFT: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTATION NUMBER: 30,727
REFERENCE/COCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1500
INFORMATION FOR SEQ 10 NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08464052; Patent No. 6008201; GENERAL INFORMATION:
APPLICANT: RILEY M.D., Lee W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 CATGCCGTCGTATTGCTG 172
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LENGTH: 1535 base pairs
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                                                                                                                                                                                                                                                                                                        650 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
SDNESS: double
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ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
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NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
RECISTRATION NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEMAN: (716,253-1600
TELEMAN: (716)-263-1600
INFORMATION FOR SEQ II NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Michael L. Goldman
STREEF: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                 NAME: Goldman, Michael L.
REGISTRATION NUMHER: 30,727
REPRENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHAKACTERISTICS:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/689,411 FILING DATE: CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application PC/TUS9409863; GENERAL INFORMATION:
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100.0%;
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                                                                                                                                                    Floppy disk
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: double
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                                                                                                          ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                     New York
: U.S.A.
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                STREET: CALL
TITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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PCT-US94-09863-1/c
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                                                                   STATE: Ne
COUNTRY:
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APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    NESULT 5
US-08-461-002-1/c
US-08-461-002-1/c
Sequence 1, Application US/08461002
Sequence 1, Application US/08461002
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
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         Query Match 100.0%; Score 18; DB 3; Length 1535; Best Local Similarity 100.0%; Pred. No. 0.84; Matches 18; Conservative 0; Mismatches no. really
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERNCE/COCKET NUMBER: 19603/186 (D-1485B)
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ROCHESCO-COUNTRY:
STATE: New York
COUNTRY: U.S.A.
2.IP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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Sequence 1, Application US/08689411

; Patent No. 6224881

; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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STREET: C11...

TTY: Rochester
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-461-002-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RITEY, Lee W. TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR PITLE OF INVENTION: DITAKE OF BYCOBALTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
COMPUTER: 1BM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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OTHER INFORMATION: CDC 1551

TOTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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GENERAL INCORNATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHOTER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PARCHILL V-1.2.1
                                                 APPLICANT: WHITE, OWER R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: WIBERCULOSIS
TITLE OF INVENTION: WIBERCULOSIS
TITLE OF INVENTION: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATEHLING DATE: 1998-06-24
SOFTWARE: PATEHLING VEF: 2.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

100.0%; Score 18; DB 4; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 4; Length 4411529; 100.0%; Pred. No. 1.1;
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Patent No. 554553
GENERAL INFORMATION:
GENERAL GOLSCHICCH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCCANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/09103840A; Patent No. 6294328
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                                   APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 catgeegtegtatigetg 18
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Best Local Similarity
           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        LENC.H: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08390878

Patent No. 5700683

GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VRULENCE-ATTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: Floor
CITY: San Francisco
STREET: Floor
CITY: San Francisco
STREET: California ...
COUNTRY: USA
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                                                                                                                                                                                                Length 1535;
                                                                                                                                                                                             100.0%; Score 18; DB 5; Length 15
100.0%; Pred. No. 0.84;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPASSORS
SOFTWARE: PSTENDIN PC-DOS/MS-DOS
SOFTWARE: PSTENDIN DATA:
CURKENT APPLICATION DATA:
FILING DATE: 17-FEB 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOKNEY ASSISTANCE: ADM
NAME: HUNTER: TOM
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09103840A
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: DNA (genomic) US-08-390-878-18
                                                           STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-09863-1
                                                                                                                                                                                                                                                                                                                  1074 CATGCCGTCGTATTGCTG 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 12412 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       705 CATGCCGTCGTATTGCTG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 catgccgtcgtattgctg 18
                                                                                                                                                                                                                                                                                        1 catgeegtegtattgetg 18
                          1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-390-878-18/c
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Sequence 1, Application US/08683426 Patent No. 5705367 GENERAL INFORMATION:
                                                                                           STREET: 411 Hackensack Avenue
CITY: Hackensack
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 2 atgreatestates 18 | HILLH | HILLH
                                                                                                                                                                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Commentative
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INFORMATION FOR SEQ 10 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 343 1684
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
      NUMBER OF SEQUENCES:
                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: COS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U. Z.IP: 07601
                                                                                                                                                                                                                               07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                           STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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APPLICANT: GOLSCHLICh, Emil C.
APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF INVERTION: GLYCOSYLITRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 1; Length 5859; Pred. No. 19;
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                                                                                                                                                                                                                                                                                        COMPUTER FRANCHEL FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 1894
CLASSIFICATION: 1994
CLASSIFICATION: A35
ATORNEY, CENT INFORMATION:
NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 600-1-095
REFERENCE/COCKET NUMBER: 600-1-095
TELEPHONE: 201 487-5800
TELEPAN: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CRARACTERISTICS:
LENGTH: 5859 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neisseria gonorrheae
                                                                                                        ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 94.1
Matches 16; Conservative
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3322..4335
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4354..5196
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445..1491
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                          STATE: New Jersey COUNTRY: USA ZIP: 07601
                                                                                                                                                                               Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: F62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-312-387B-1
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APPLICANT: GOLSCHLICH, EMIL C.
TITLE OF LIVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85,68; Score 15,4; DB 1; Length 5859; 94,18; Pred, No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: HIM PC compatible
COMPUTER: HIM SYSTEM: PC-NOS/MS-LNS
SOPTWARE: Pedentin Release #1.0, Version #1.25
COMPUTER: 16M PC compatible
OPERATING SYSTEM: PC-DOS/MS-INOS
SUFFMARE: Patentin Release #1.0, Version #1.25
SUFFMARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGGNT INFORMATION:
                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRAFION NUMBER: 26,742
REFERENCE/Docket NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Neisseria genorrheae
STRAIN: P62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET 411 Hackensack Avenue CITY: Hackensack
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18-08-683-458-1
| Sequence 1, Application US/08683458 |
| Sequence 1, Application US/08683458 |
| Patent No. 5798233 |
| Patent No. 57982410: |
| GENERAL INFORMATION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Klauber & Jackson STREET: All Hackensack Avenue |
| STREET: Hackensack Avenue |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 5859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ihm PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC 'COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION 197A:
APPLICATION 197A:
APPLICATION NUMBER: US/08/683,426
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                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION INTRA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 516
ATTORNEY/AGENT INFURWATION:
NAME: JACKSON ESG, DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
FELECOMMUNICATION INFORMATION:
TELEFAX: 201 343-1684
INFORMATION FOK SEQ 10 NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5859 base; pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA (yenomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 2796 ArdeedeestAffecte 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1491..2330
; OTHER INFORMATION: 1gtB
US-08-683-426-7
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STRANDEDNESS: both
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New Jersey
COUNTRY: USA
New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: F62
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Sequence 7, Application US/08683426

Sequence 7, Application US/08683426

Patent No. 5705367

GENERAL INFORMATION:

APPLICANT: Gotschlich, Emil C.

TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEB: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 1; Length 5859; pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1..381
OTHER INFORMATION: 91ys (91ycyl tRNA syntetase beta chain)
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                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION DATA:
PILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5801
TELEPHONE: 201 343-1684
TELEFA: 13521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACPERISTICS:
LENGTH: 5859 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: UNROWN MOLECULE TYPE: UNROWN HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Neisseria gonorrheae STRAIN: F62
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94.1%;
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LOCATION: 4354..5196
OTHER INFORMATION: 19tE
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LOCATION: 445..1491
OTHER INFORMATION: 19tA
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OTHER INFORMATION: 19tD
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OTHER INFORMATION: 19tC
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Best Local Similarity 94.1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,458
FILING DATE: SEPTION: 435
CLASSIFICATION NUMBER: 08/312,387
FILING DATE: SEPTION: 435
CLASSIFICATION NUMBER: 08/312,387
FILING DATE: SEPTION: 435
CLASSIFICATION: 435
CLASSIFICATION NUMBER: 26,742
NAME: JACKET INFORMATION: 1000
NAME: JACKET INFORMATION: 1000
TELEFAX: 13521
TELEFAX: 201 48'-5800
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85.6%; Score 15.4; DB 1; Length 5859;
Best Local Similarity 94.1%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0
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Search completed: April 3, 2002, 08:12:53 Job time: 42533 sec

15 83.3 377 13 18 82.2 128 10 18 82.2 315 13 18 82.2 383 11 18 82.2 383 11 18 82.2 395 10 18 82.2 410 11 18 82.2 425 10	23 14.8 82.2 434 10 BE024649 24 14.8 82.2 464 10 BE024867 25 14.8 82.2 479 11 BF844800 26 14.8 82.2 486 10 AA314278 27 14.8 82.2 493 11 B6733499 29 14.8 82.2 505 11 H11823 29 14.8 82.2 523 11 B7728035 30 14.8 82.2 523 11 B7728035	14.8 82.2 534 13 A0555508 14.8 82.2 534 13 A0555508 14.8 82.2 604 13 A0970996 14.8 82.2 640 10 AW954845 14.8 82.2 660 11 BG58511 14.8 82.2 666 10 AU34159 14.8 82.2 701 11 BG60192 14.8 82.2 701 13 BH110072	14.8 82.2 742 13 A0250765 14.8 82.2 780 11 BF942570 14.8 82.2 790 10 AW940B55 14.8 82.2 844 13 AZ129739 14.8 82.2 924 11 BG028677	RESULT 1 CNSO2LR5/c LOCUS LOCUS LOCUS DEFINITION Tetraodon nigroviridis genomic survey sequence T7 end of clone 148A13 of library G from Tetraodon nigroviridis, genomic survey sequence. ACCESSION AL20316.2 AL20316.2 AL20316.2 CSS 14-MAY-2000 Clone 148A13 of library G from Tetraodon nigroviridis, genomic survey sequence. AL20316.2 AL20316.2 AL20316.3 AL20316.3 CSS 14-MAY-2000 CSOURCE TETRAODON NIGROVIRIDIS. SOURCE TETRAODON NIGROVIRIDIS. ORGANISM TETRAODON NIGROVIRIDIS. ENRARYOTE: Chordata; Craniata; Euteleostomi;		REFERENCE AUTHORS ROEST-Crollius.H., Jaillon.O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. TITLE Human gene number estimate provided by genome wide analysis using TITLE Tetradoon nigroviridis DNA sequence JOURNAL Unpublished AUTHORS Genosope. TITLE Direct Submission JOURNAL Sequence is a single read and was generated as part of a large Scale clone-end sequencing project of the Tetraodon nigroviridis
GenCore version 4.5  yright (c) 1993 - 2000 Compugen Ltd.  search, using sw model  1 2, 2002, 21:48:01; Search time 3835.7 Seconds 50.427 Million cell updates/sec	-4 attgctg 18 3apext 1.0	. F 5 0 4	:* em_estfun:* em_esthum:* em_estin:* em_eston:* em_estpl:* em_estpl:* em_estpl:* em_estpl:*	em_tc:*  em_tc:*  gb_est:*  gb_est:**  gb_est:**  em_gss_tun:*  em_gss_lun:*  em_gss_pln:*  em_gss_pln:*  em_gss_pln:*  em_gss_pln:*  em_gss_pln:*  em_gss_pln:*	em_gss_orner:* e number of results predicted by chance to have a han or equal to the score of the result being printed, by analysis of the total score distribution.  SUMMARIES Length DB ID	3 CNSO2LR5 3 CNSO2LR5 0 AU060300 0 AU06178 1 N93955 1 N93955 0 BE775420 0 AW93449 0 A1403760 0 BE777156
Copyright OM nucleic - nucleic search Run on: April 2,	Title: US-09-785-904 Perfect score: 18 Sequence: 1 catgccgtcgt. Scoring table: IDENTITY_NUC Gapop 10.0 , (Searched: 11351937 segs	mber of hits sember of hits semble seq length: DB seq length: cessing: Minimuter Maximuter		8: em_estov: 9: em_htc:* 10: gb_est1: 11: gb_est2: 12: gb_htc:* 13: gb_dss:* 14: em_gss_f* 15: em_gss_h 16: em_gss_p 18: em_gss_p 18: em_gss_p 18: em_gss_p 19: em_gss_p	<u>ም</u> ታ ም	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

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GSS; genome survey sequence.

Fetraodon nigroviridis.

Tetraodon nigroviridis.

Tetraodon nigroviridis.

Actinoperaydi; Neopteryqii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthoperaydii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontiformes; Tetraodontidae; Tetraodontiformes; Tetraodontidae; Tetraodontiformes; Tetraodontidae; Tetraodontiformes; Secartoridis, Tetraodontiformes; Secartoridis, Tetraodontiformes; Messendau, L. Jaillault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Bernot, A., and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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/note="Genoscope sequence ID : C0AG145CD08LP1-end : T7"
/note="Genoscope sequence ID : C0AG145CD08LP1-end : T7"
/ 291 c 255 g 243 t 9 others
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t     4 others
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Tetraodon nigroviridis genome survey sequence T7 end of clone
145H15 of library G from Tetraodon nigroviridis, genomic survey
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
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/db_xref="taxon:99883"
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Pred. No. 3.8e+02;
0; Mismatches 1;
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Pred. No. 3.6e+02;
0; Mismatches 1;
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178 c 268 g 142
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ilarity 94.48;
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Dictyostellum discoideum.
Dictyostellum discoideum.
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 312)
Morlo, T., Urushihara, H., Salto, T., Ugawa, Y., Wizuno, H., Yoshida, M., Yoshino, R., Mitza, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental CDNA in Dictyostellum discoideum
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1 (bases 1 to 252)
Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Voshino,R., Mitra,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maedda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
Developmental CDNA in Dictyostelium discoideum
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AU061778
AU060300 252 bp mRNA EST 20-MAY-1999 AU060300 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLJ109, mRNA sequence.
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/dev_stage="slug"
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Unpublished (1998)
Contact: Hideko Urushihara
Contact: Hideko Urushihara
University of Fiological Sciences
3.3.10 Ten-nodal, Tsukuba
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
                                                                                                                                                                                                                                                                                                                                                                   Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: 4402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
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/organism="Dictyostellum discoideum"
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/db_xref="taxon:44689"
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1 (bases I to 468)

2 (bissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., More, M., Morla, M., Marsons, J., Pranqe, C., Rifkin, L., Kohlfing, T., Golellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Treevaskis, E., Gencaration and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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/Jab_host="Diversity"
/Jab_host="Drign" | Jab_host="Drign" | Jap_host="Drign" | Jap_ho
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                                                                                            /strain="AX4"
/db_xref="teaxon:44689"
/clone="sLr846"
/clone_lib="Dictyostellum discoideum SL (H.Urushihara)"
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Insert Length: 480 Std Error: 0.00
Seq primer: mbD.REGA+ET
High quality sequence stop: 223.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                         Length 332;
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/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                               /organism~"Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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Pred. No. 9.6e+02;
); Mismatches 1;
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/db_xref="GDB:1252750"
/db_xref="taxon:9606"
Location/Qualifiers
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94.1%;
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Fax: 314 286 1810
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1 (bases 1 to 490)

Morlo, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yushida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Unpublished (1998)
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Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W." 6 there
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AU061934 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
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/dov.stage="slud"
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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Pred. No. 1e+03;
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Institute of Biological Sciences
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/db_xref-"taxon:44689"
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AQ179545.1 GI:3576912
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88.9%;
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MY-02-G-06 PinfestansMY Phytophthora infestans cDNA, mkNA sequence.
BE778420
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Phytopathology
Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="Plate=3177 Col=7 Row=I"
/clone="Plate=3177 Col=7 Row=I"
/clone=Ib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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Kamoun, S., Harber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F. Initial assessment of gene diversity for the comycete pathogen Phytophthora infestans based on expressed sequences Fungal Genet. Biol. 28 (2), 94-106 (1999)

Contact: Govers F
                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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/strain="DBR7602" Al mating type"
/db_xref="taxon:4787"
/clone_lib="PinfestansMx"
/dev_stage="4-week old vegetative, non-sporulating
mycellum in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potato late blight agent.
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceac;
                                                                         Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 508;
                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 (206) 616-3887
Fax: (206) 616-3887
Famil: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3177 row: I column: 7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 others
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    529
    /organism="Phytophthora infestans"

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ilarity 94.1%; Pred. No. 1e+03;
Conservative 0; Mismatches 1;
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hausen,T., Craven,M.B., Bowman,C.L., Ahn,S., Konning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue (Upublished (1999)
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; Total RNA was isolated from mycelium of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelii) and the successive number of the microtiter plate (e.g. MY-06-A-04)."
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/organism="Drosophila melanogaster"
/db_xref="Laxon:727"
/clone="GH23256":727"
/clone="GH23256":727"
/clone="Lib="GH3256":727"
/sex="male and female"
/dev_stage="adult"
/lab_host="0H5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2: XhOI: Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
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MY-25-B-07 PinfestansMY Phytophthora infestans CDNA, mkNA sequence.
BE777156
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Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 640)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsaug, G., Enexis, S. and Rubin, G.M.
BDCP/HMI Drosophila EST Project
Unpublished (2001)
     AI403760 640 bp mRNA EST 19-APR-2001 GH23265.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH23265 5prime, mRNA sequence. AI403760
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Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.
Initial assessment of gene diversity for the comycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/FST, estefruitfly.berkeley.cdu Plate: 232 row: F column: 5 High quality sequence stop: 438. Location/Qualifiers
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Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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Pred. No. 1.1e+03;
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                                                                                          AI403760.1 GI:4246847
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Contact: Govers F
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/strain="Cc-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/dlone_lib-"C. reinhardtii CC-1690, Stress condition I,
/clone_lib-"C. reinhardtii CC-1690, Stress condition I,
/note="Vector: pBluescript II SK-; Site_I: Ecoki; Site_2:
/note="Vector: pBluescript II SK-; Site_I: Ecoki; Site_2:
/note="This library, constructed by John Davies and Jeffrey
/mcDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP- (4hr, 12hr, 24hr), NO3 to NH4 (40min, 1hr,
/hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mkNA was
/purified from each sample, pooled and CDNA yputus:i.cel.
/the cDNA was directionally cloned into lambda Zap HI
/the cDNA was directionally cloned into lambda Zap HI
/the cDNA was directionally cloned into lambda Zap HI
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Chlamydomonas reinhardiii.
Eukaryota, Viridiplantae: Chlorophyta, Chlorophyceae, Volvocales, Chlamydomonadaceae, Chlamydomonas.
Chlamydomonadaceae, Chlamydomonas.
B (bases 1 to 2051)
Chassanin, A., Davies, J., Ferenspiel, N., Barris, E., Hauser, C., Roberte, C., Silliow, C., and Stern, D., Univertula: System for analyzing Gene Function and Requirition in Vascular Francis; project plass 3
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963101A02.x1 C. reinhardtii CC-1690, Stress condition J. normalized Lambda Zap 11 Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Pred. No. 1.1e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                  /organism="Phytophthora infestans"
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
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Tel: 919-613-8159
Fax: 919-613-8177
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BASE COUNT ORIGIN

us-09-785-904-4.rst

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Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading
                                                                                                                                                       AV834783 575 bp mRNA EST 22-JUN-2001
AV834783 K. Sato unpublished cDNA library: Hordeum vulgarc subsp.
spontaneum top three leaves adult, heading stage Hordeum vulgare
subsp. spontaneum cDNA clone bahl5n23, mRNA sequence.
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cb01a01_p1 ZF adult heart library Danio rerio cDNA 5 prime, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Cuto 2-20-1. Kursahiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct submission:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             database:http://www.shiqen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
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Expressed Sequences from The Adult Zebrafish Heart
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/dev_stage~"adult, heading stage"
160 c 154 g 119 t
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Hordeum vulgare subsp. spontaneum
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/clone="bahl5n23"
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pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bondo et al (1996) Genome Research 6: 791-806."

461 c 551 g 294 t 167 others
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RFCI-24-333F5.TVB RPCI-24 Mus musculus genomic clone RPCI-24-333F5,
BH100992
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other, GSSs: RPCI-24-333FS. TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from HACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww.ilgr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 333 row: F column: 5
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RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBACI cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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100.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 0;
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COMMENT

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Gaps

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FEATURES

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Contact: Mark C. Fishman
Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 617726580
Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
http://zebrafish.mgh.harvard.edu
http://zebrafish.mgh.harvard.edu
http://zebrafish.mgh.harvard.edu
http://zebrafish.mgh.harvard.edu
http://zebrafish.mgh.harvard.edu
rhe original clones used for sequencing are no longer available;
the library is available from Mark C. Fishman.
Insert Length: 128 Std Error: 0.00
Seq primer: Pl.
Location/Qualifiers
ince /organism="Danio rerio"
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/note="Organ: heart; Vector: LambdaZAPII; Site_1: EcoRI;
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82.2%; Score 14.8; DB 10; Length 128;
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		650 bp DNA	Sequence 5 from patent US 6008201.		.0025753					550)		DNA molecule encoding for cellular uptake of	d uses thereof	Patent: US 6008201-A 5 28-DEC-1999;	Location/Qualifiers	0	/orqanism="unknown"	258 c 185 g 84 t	
		AR096715 65	Sequence 5 from	AR096715	AR096715.1 GI:10025753		Unknown.	Unknown.	Unclassified.	1 (bases 1 to 650)	Riley, L.W.	DNA molecule end	tuberculosis and uses thereof	Patent: US 60082	Locatic		/ordani	123 a 258	
RESULT 1	AR096715	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE		JOURNAL	FEATURES	source		BASE COUNT	

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Riley, L.W. and Chong, P.
Riley, L.W. and Chong, P.
DNA molecule fragments encoding for cellular uptake of
Mycobacterium tubérculosis and uses thereof
Patent: 18 6224881-A 5 01-MAY-2001;
Location/Qualifiers
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Length 650;
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100.0%; Pred. No. 4.9e-78;
Live 0; Mismatches 0;
38.9%; Score 176; DB 6; I
100.0%; Pred. No. 4.9e-78;
ive 0; Mismatches 0;
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Sequence 1 from patent US 6008201
AR096713
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258 c 185 g
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Sequence 5 from patent US
AR147696
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Riley, L.W.
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Matches 176; Conservative
              Best Local Similarity 100.
Matches 176; Conservative
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AR096713
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Mycobacterium bovis BCG DNA flanking deletion region 3.
035021
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Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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1 (bases 1 to 1535)
Rilev,L.W. and Chony,P.
MAN molecule fragments encoding for cellular uptake of
Mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 101-MAY-2001;
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100,0%; Pred. No. 4.2e-78;
ive 0; Mismatches 0;
                                                                            38.9%; score 176; DB 6; L. 100.0%; Pred. No. 4.2e-78; ive 0; Mismatches 0;
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AR147694
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544 c 458 g
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1. .1535
                       /organism="unknown"
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    1 (bases 1 to 1604)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium
bovis ECG and virulent M. bovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                          Joses 1 to 1604)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Birect Submission
Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of Medicine, Yeunganam University, 317-1, Daemyungdong, Namku, Taegu 705-035, South Korea 3 (bases 1 to 3453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (14-AUG-1997) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein
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                                                                                                                                                                                                                                                                                                                                                              /note="site of deletion breakpoint in this organism.
Virulent M. bovis has additional 10 kbp at this site"
637 c 416 g 214 t
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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100.0%; Pred. No. 4.1e-78;
ive 0; Mismatches 0; Indels
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/db_xref="taxon:1765"
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Location/Qualifiers
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Matches 176; Conservative
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Direct Submission
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/codon_start=1
/transl_table=11
/protein_id="AAR66649.1"
/the xrel="GI:2326951"
/the xrel="GI:2326951"
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/the xrel="GI:2326951"
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ADVEDATKLVQGDITDAELVSQLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTF
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WYSELCVRAATISNCSNNYGPYQHVER FIPROLTNCLIKCLIKYGDGGWYRDMIHYDDH
NSAVRRILDRGRIGETYLISSEGERDNLTVLRSLIRLMBRDPDDFDHYTDRVAHDLRY
AIDPSRLYDELCWAPKHTDFERALRTTIDWYRDNESWLASLKHAGGRYODAGO"
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ADVEDAIRLVQGDITDAELVSQLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTF
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WYSLICVERTISNCSNNYGPYQHVER FTROTTNCLTGLLKLYGDGGWYRDMIHYDDH
NSAVRRILDRGRIGETYLISSEGERDNLTVLRSLLRLMBRDPDDFDHYTDRVAHDLRY
AIDPSRLYDELCWAGFTYLSSEGERDNLTVLRSLLRLMBRDPDFFFHYTDRVAHDLRY
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VLLJDQDRNTYVSDGLAHGFLALQDNSTVMYLCSAEYNPQRQHTTCATDPTLASTRRW
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7002. 2655
7001cm-3-4 copies in M. tuberculosis genome; Found in the rfb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv, tubers, Eddman, and many isolates; not found in M. smegmatis & M. avium."
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/protein_id="AAB66647.1"
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                                                     /organism="Mycobacterium tuberculosis'
/db_xref="taxon:1773"
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150. 1139
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100.0%; Pred. No. 3.5e-78;
live 0; Mismatches 0;
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/rpt_unit=1806. 229
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1136. .1747
/gene="rmlC"
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150. .1139
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/transl_table=11
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/3002. 3772
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/gene="MT0096"
1449. .2123
/qene="MT0096"
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/gene="MT0099"
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2280, .2873
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                                           laboratory strains
Unpublished
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                                                                           REFERENCE
                                                              JURNAL
                                                                                              AUTHORS
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                               TITLE
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0
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Actinomycetales; Corynebacterineae: Mycobacteriaceae;
Mycobacterium: Mycobacterium tuberculosis complex.

1 (bases 1 to 9281)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium bovis BCG and virulent M. bovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                                                                                                                                                                                                                                                           Journal 10 9281)
2 (bases 1 to 9281)
3 (bases 1.0. Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Mahairas,G.G., Sabo,P.J., Hickey, M.J., Singh,D.C. and Stover,C.K. Submitsed (29-AUG-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White, 0.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mycobacterium bovis"
/db_xref="taxon:1765"

misc_difference replace(1400. .>9281,"")
/note="absent in related avirulent strain M. bovis BCG"

COUNT 1706 a 3191 c 2929 g 1453 t 2 others
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I (bases 1 to 9764)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
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                                                                                                                                    end.
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100.0%; Pred. No. 2.9e-78;
iive 0; Mismatches 0;
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                                                                                                       MBDR3S1 9281 bp DNA
Mycobacterium bovis deletion region 3,
035017
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Location/Qualifiers
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Mycobacterium bovis
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AE006921 AE000516
AE006921.1 GI:138
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Best Local Similarity
Matches 176; Conserv
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KEYWORDS
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/translation="naknonnirneelitcglgghytyapddaalaaklrastglge
vwrclrcgdpalggpggrgapedaplimrgallganiirlalgyerlyablyllalaam
vwreprgargaturblylraagfyvdomtyihaleralaakpstlalitgmla
ayavloaveovglwilrkwgeyfavvatsffelevhblakgitttryvyfsinvaav
vyilliskrlegyrggrkaydverrgeglldleraamlt"
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/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="AAK44319.1"
/db_xref="01:18879143"
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REPERANKPOFOTGOLGOPROBMTVTVVDAGPGRVSRSVEVAAPAAELFA1VADGPRRH
ELDGSGTVRONIKPYRCTYRGIOGRGDMTVTVVDAGPGRVSRSVEVAAPAAFAELFA1VADGFRRH
RWRWEFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
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TALSRLGGLVTPGGTILAVYTFVTPSLRNGLMHLTSWVACGMANRVKGKWEHSAPIKWP
PPQTLHELRSHVRALLPGACIRRLLYGRVLVTWRAPV"
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Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MT0095"
//gene="This region contains an authentic point mutation,
//oute="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact; similar to SP:
                                                                                                                                                                                                                                                                                                  "The factor of the state of the
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/strain="CDC1551"
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/qene="MT0098"
/hore="similar to GP:145427; identitied by
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/protein_id="AAK44321.1"
/db_xref="G1:13879145"
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/protein_id-"AAK44320.1"
/db_xref="GI:13879144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:83331"
/note="clinical strain"
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CDS

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/translation="miwl.hpogdltpterarkrgitl.snooydcmski.sgyllppdara
TFEAVLAKLAAPGATRUDDHTPVIDTPDAAAIDROTRSQAGKNHDGI.AGLRALIAS
GKLGGNGGLTGGTLI.PMLGTGAGGGFTGGGTLI.PMADVI NHTSHAHIYSPASGR
YPQAIFPDHGTPLALYTITKRIASPAGRIMLFANDRGCTKFGCDAPATHSQAHIHYTAWTS
TGKTDITELTLAGGPUNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQPHTNTFHHPERF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not the result of a sequencing artifact; identified by doliments, putative, conserved hypothetical protein, althenic frameshift."

13103 c 3360 g 1748 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8956...9623)
/gene="MT0104"
/note="This region contains an authentic frame shift
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacterium; Mycobacterium; Mycobacterium; Ucbacterium; Tuberculosis complex.
I (bases I to 10019)
Yu,S. and Jacobs,W.R. Jr.
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                                                                                                                                            /product="conserved hypothetical protein"
/protein_id-"AAK44326.1"
/db_xref-"G1:13879150"
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                                                     /note="identified by Glimmer2; putative"
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    11. 10019
    /organism="Mycobacterium bovis BCG"

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complement(8232. .9095)
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                                                                                                                        /transl_table=11
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                                                                                             /codon_start≃l
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Aak44323.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="cation-transporting ATPase, E1-E2 family"
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                                                                                                    by Glimmer2; putative"
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complement(7337. .8185)
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CGPHLAPAPWANSLPGWTAHVTLARRVGGHQLGRALRIAGRPSRINGRFAGLRRWDG
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LytalcinachaponavVyrdooperation
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adenosyImethionine-8-amino-7-oxononanoate
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section 114 of 280 of the
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Pred. No. 2.9e-78;
0; Mismatches 0;
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100.0%; Pred. No. 2.7e-78;
Live 0; Mismatches 0;
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1. .12412
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Conservative 0;
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AHHYSPASGKYPQATPDHGTPLALYHTRIASPAQRTMLFANDKGCTKPGGDAPAYHS
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CLVRRLPAVGHTLINQLDTQASEEELGGTLCCALANRLRITKPDAAI.RTADAADLGPR
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SRSISSRRAGPLRPAGHGLATPRRRPHRHRTRPQTRHHPEQPAIRKHVTAKWLPDPPS
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                                                                                                                                                                                                 Fleischmann, R.D., Alland, D., Elsen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberq, S.L., Delcher, A., Uterback, T., Weidman, J., Kkouri, H., Gill, J., Mikula, A. and Bishai, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers 1. 17783 /organism-"Mycobacterium tuberculosis CDC1551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished

2 (bases 1 to 17783)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Peterson, J. F., Nelson, W.C., Umayam, L.A., Ermolacva, M., Kouri, H., Coloney, J.F., Nelson, W.C., Uterback, T., Weidman, J., Khouri, H.,
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Mycobacterium; Mycobacterium tuberculosis complex.
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Gill, ", Mikula, A. and Bishal, W.
Direct Submission
Submitted (25-APR-2001) The Institute
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Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
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LIKVLHDGTAVTGLLVVRPDGCGIISAPSVILATGGLGHLYSATTNPAGSTGDGIALGL
WAGVAVSDLEFIQFHPTMLFAGRAGGRRPLITEAIRGEGAILVDKQGNSITAGVHPMG
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VVPCAHY SCCGI VTUVYGOTELLGI YAAGBVARTGI HGANRI ASNSI LI EGI JVVGGRAG
KAAAAHAAAGGRSKATSSATWEPI ISYTALDRGDLQRAMSRDASMY RAAAGLHRLCDS
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                                                                                                                                                         /note="similar to SP:P11458 GB:X12713 PID:581137 GB:U00096
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Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.
295586 AL123456
29586.1 GI:3261785
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thes 0;
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9021. 990?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7468. .9051
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7468. .9051
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ACCESSION
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EGWAVSVPDHEGPKGLWGSPYEPGYRVLDGIRAALNSERVGLSPATPIGLWGYSGGGL
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RLRYGALDFOTVPLE, REGDHALTY VTQAPPVFFARRPLQIALTLMWPAGIASLVAALLA
AGTARDDLGGYPAVDPSSNARTEALETPQAPVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASAWAAEACGEYAPDLDIVGAVLGSPVGDLGHTFRRLNGTLLAGLPALVVAALQHSYP
GLARVIKEHANDEGRQLLEQLTEMTTVDAVIRWAGRDMGDFLDEPLEDILSTPEVSHV
FGDTKLGSAVPTPPVLIVQAVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSL
KSAWLDIPSLVEAAKQTAKSGATEFCIVAAVRGPDERLMAQVAAGIEAIRNEVEINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPLSAPMTLRWLTDRFAGKPLTDHRVRTTWPTIFNPMTYAGMAKLAVIAAKVITGRKL
SRRPL"
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                                                                                                                                                                                                                                  /note="identified by Glimmer2; putative
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3317. .3898
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2997. 3036
                                                                                                                                                                              2997. .3236
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787 397 727

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
subroulosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2117233.
                                                                                                   Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 32437)

1 (cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C. E., Tekia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Imalin, W. Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, S., Murphy, L., Oliver, S., Osborne, J., Quall, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             betails of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.%anger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in Tapparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon gaty, gty, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deciphering the biology of Mycobacterium tuberculosis from the
                                                        Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .32437
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/db_xref="taxon:83332"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence
Nature. 393 (6685), 537-544 (1998)
                          Mycobacterium tuberculosis H37Rv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 32437)
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TITLE
JOURNAL
                                                               ORGANISM
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AUTHORS
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KEYWORDS
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/codon\_start=1

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/note--Rv1568, (MTCY336.35c), bioA, len: 437. Function: probable adenosylmethionine-8-amino-7-oxononanoate aminotransferase (ECZ.6.1.62) 006622. Contains aminotransferase class-III pyridoxal-phosphate attachment site (PS00600). FASTAresults, BIOA_MYCLE P4548 (436 aa) opt: 2534; E(): 0; 85.1%identityin 436 aa overlap. Also similar to other M. tuberculosis proteins e.g. MTCY27.12c, (449 aa). FASTA score: E():3.5e-16; 29.5% identity in 421 aa overlap. TBparse scoreis0.874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probably exported has QOAPV repeats at C-terminus, similar to hypothetical M. leprae protein, to putative invasins 1.2(00739), 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_LISMO P21171. FASTA results, 049634 COSMID BHITO (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlap. TBparse sccreis 0.890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110GVKEEPPGWALVPVGGATMLMILAGANRQGHPGTRRRELPILANRLLATAPLVALGAMA
YSWYLWHWPLLI FWLSYTGHRHANFYTGAAVLLVSGILAYLTTRLVEDPLAKRARAGY
SRDAAVPD IPPRRLERPRTIVIGSOVACH, GAGALLATATSFTWREHVIVORAAGKELSGIS
SRDYPGARALIDHYRYPKLRRRPTVLE, TAGDLPTSTROGGISPFWRAI INGTYGDVD
APRTIALAGGSHAEHWLTALDLLGRRHHFKVVTY IKMGCPLSTEVPLINGNNAPY PO
GHWOQAAMARIADHHYRYPTSTRRPWIIKPGDOWPATYGI WOTFADNII PVLAMR
DIPPMLVKDGOPF IPADCLAKGGNPOGSGIABEKVLUDRNPTILDFVAHRPLLKPLDMS
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                                                                                                                                  /translation="MLTLSPPRPPALTPEPALPPVTMGTRTTGFYRHDLDGLRGVAIA
LVAVFHVWFGRVSGGVDVFLALSGFFFGGKTLRAALNPDLSLSPIAEVIRLIRRLLPA
                                                                                                                                                                                                         LVVVLAGCALLTIAIQPQTRWEAFANQSLASLGYYQNWELASTVSNYLRAGEAVSPLQ
                                                                                                                                                                                                                                        HIWSMSYQGOFYLAFLLLVAGCAYLLRRLFRGPRAPYLRTMFVVLLSTIJTIASFIYAI
VAHHAYQATAYYNJFARAWELLAGALVGAVVPHVRWPMMLRTAVATAALAAILSCGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2327. .3019)
/gene="Rv1566c"
/note="Rv1566c, (MTCY336.37), len: 230. Function: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-'possible RBS, AAGAGG, for Rv1566c" complement(3258. 3263) complement(3258. 3263) biote-"ASNI site: ATTAAT: probably linking fragments Biogs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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/protein_id="CA6090072.1"
/db_xref="G1:211727"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comptement (329, 3543)
Agene "Rv1567c"
complement (3259, 3543)
/gene="Rv1567c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2327. .3019)
/gene="Rv1566c"
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/gene="bioA"
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/db_xref="SPTREMBL:Q10881"
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                                                        ORGANISM
                                                                                                                                          REFERENCE
                                                                                                                                                           AUTHORS
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                KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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VERSION
                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:006621"
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LEADNDYLGLSERPAVIDGYQALRINGAATGSTLVTGDTKLHQQPEAELAEVGAAA
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AALRSRDEQRAVVVTDSVFSADGSLAPVRELLEVCRRHGALLLVDEAHGLGVRGGGRG
LLYELGLAGAAPDVWTTLSKALGSQGGVVLGPTPVRAHILDAARPFIPT
                                                                                                                                                    LAKLLVDITPAGLDTVFFSDSGSVSVEVAAKMALQYWRGRGLPGKRRLMTWRGGYHGD
TFLAMSICDPHGGMHSLWTDVLAAQVFAPQVPRDYDPAYSAAFEAQLAQHAGELAAVV
VEPVVQGAGGMRFHDPRYLHDLRDICRRYEVLLIFDEIATGFGRTGALFAADHAGVSP
                                                                                                                                                                                                                 DIMCVGKALTGGYLSLAATLCTADVAHTISAGAAGAI.MHGPTFMANPLACAVSVASVE
LLLGQDWRTRITELAAGLTAGLDTARALPAVTDVRVCGAIGVIECURPVDLAVATPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAARAALRVLQAEPWRPQAVLNHAGELARMCGVAAVPDSAMYSVILGEPESAVAAAA
CLDAGVKVGCFRPPTVPAGTSRLRITARASLNAGELELARRVLTDVLAVARR"
5806. .5835
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Rv1569, (MTCY336.34c), biof, len: 386. Function: probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 00661. Contains aminotransferases class-1f pyridoxal-phosphate attendment site (PS00599). FASTA results, BIOF_MYCLE P45487(385 aa) opt: 1971; E(): 0; 80.1% identity in 381 aa overlap. Also similar to MTCY10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTCY251 38380 bp DNA BCT 03-AUG-2001
Mycobacterium tuberculosis H37Rv complete genome; segment 5/162.
274410 AL123456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgcgggccacctttgaagccgtgctagccaaactggccgcccccggcgaccaaccccg 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                  /note="PS00600 Aminotransferases class-III
pyridoxal-phosphate attachment site"
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pyridoxal-phosphate attachment site"
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                                                    /protein_id="CAB09069.1"
/db_xref="GI:2117269"
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5101. 6261
                                                                                                                                                                                                                                                                            4541. .4654
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/gene="bioD"
6258. .6938
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bioF"
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LOCUS
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Actinomycelales, Actinobacteria, Actinobacteridae;
Actinomycelales, Corynebacterineae; Mycobacteridae;
Actinomycelales, Corynebacterineae; Mycobacteridae;
Actinomycelales, Corynebacterineae; Mycobacteridae;
Mycobacterium; Mycobacterium tuberculosis complex.

1. (bases 1 to 3830)
RS Cole, S.T., Brosch, R. Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry 111, C.E., Takaia, F., Badocok, K., Hasham, D., Brown, D., Chillingworth, T., Connor, R., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajundream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Squares, R., Sulston, J.E., Taylor, K., Whilehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(UML, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position of c. C. CAUTION: In some cases we may not have predicted the correct infitation codon. Where possible we choose an initiation codon (atq. gtg, or ttg) which is preceded by an upstream ribusome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CBIO 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:1405752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .48380
/organism "Mycobacterium tuberculosis H37kv"
/strain="H37kv"
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/strain="H37kv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature, 393 (6685), 537-544 (1998)
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/db_xref="G1:1405754"
Mycobacterium tuberculosis H37Rv.
                                      Mycobacterium tuberculosis H37Rv
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<1. .35889
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/clone="Y251"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 38380)
Parkhill, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"hycD"
6. .956
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gene

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/translation-*MOOPWAANTHYDALLDAMYPLGTQCVLDVGCCOGLLAARLARRI
PYVTAVDIDAPVLRRAQTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
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ELDGSGTVRGNIKVPAKLVVGSRFSTRAKLFGLPXRTSRVPALKPNELVEWSBPLGH
RWHWEDESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
                                                                         NAAVTGHRLLRGAI RAGGVALRALPOTDELAALAVDIAEVATUTLANSVVYDRFAGTA
VLHPDDASALGCCLGYVARASGIRSDARVEHPTIVLPITEIGAPISGIVLARYTVRRDEF
AASAALAQH IVESHTGPIEYAATLHPVGAPSSGIGIVEGWRGTIVHKVFIDVDGRITR
AKVVDPSWFNWPALPVAMADTIVPDFPLANKSFNQSVAGNDL"
                          RFSVAGETIVRLKARLMFVHRGIEKLFHGRPATAAVDLAERISGDTSAAHALAHSLAI
EDALGIELPHEVHRLRALIVELERLYNHAADLGALANDVGYSLANAHAQKIRENLLRR
RLVRHAHWPDWHPMRTDAGPAPEFTDTGAFPFLAVEGPGVYE1PVGPVHAGLIEPGHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTY13E12 43401 bp DNA BCT 03-AUG-2001 Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 z-score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //note-"R0089, (MTCY251.07), len: 197. unknown, some similarity to sp[P12999|BIOC_ECOLI BIOTIN SYNTHESIS PROTEIN BIOC. (251 aa). FASTA scores: opt: 202 z-scor 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ноте-"куннун, (МТСҮ251.08), len: 256. Unknown."
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                                                                                                                                                                                                                                                                                                          /note="Rv0088, (MTCY251.06), len: 224. Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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/note="aaqqaq, potential rbs upstream of 16158. .6928
6158. .6928
6158. .6928
6158. .6928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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/db_xref="SwISS-PROT:010886"
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Pred. No. 2.2e-78;
0; Mismatches 0;
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5436. .6029
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/qene-"Rv0090"
                                                                                                                                                                                                              /qene-"Rv0088"
4605. 5279
                                                                                                                                                                                                                                                        4605. .5279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start
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Best Local Similarity
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jobs. 1995. (MTCY251.04), oxidoreductase, len: 488, fgene="hyco" and revoluble, (MTCY251.04), oxidoreductase, len: 488, force="hyco" most similar to sple?74371HYFE_ECOL. HYDKOGRASE-4 COMPONENT FEC 1. (526 aa), FASTA scores: opt: 948 component FEC 1. (513 35.9% identity in 493 aa overlap. Also similarto E. coli 49087711 & NUOL_ECOLI P33607 nadh dehydrogenasei chain 1 (613 aa) FASTA scores, opt: 360, az.score: 354.9, E():3.2e-13, (27.9% identity in 488 aa overlap), and to NUON ECOLI P33608, nadh dehydrogenase i chain (425 aa), FASTAscores, opt: 375, z-score: 371.4, E(): 3.9e-14, (25.0% identity in 432 aa overlap)" (codon_start-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HULAHGIGKTULLAGODAHDSTANDAGOMRERALLAIADAGTTLAIAAALLLAMEASELAIGKTULAAGODAHDSTANDJIGGWRERRLIGVSFAVGLIVLIGLPPF
AMFASELARSLAHRSLAMWLGAALLLIAIGGTALANNSGRMLIGTPAAGAPAITVP
ATAAAALMYGIVVSAALGITAGPLADLIGIAASNYGLP"
ATAAAALMYGIVSAALGITAGPLADLIGIAASNYGLP"
/gene-14570
3092. 4570
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AMGEWMGSGAQFGLGGLLANDALTVVMLVVIGIVGTLATAASIGYIDTELAIGHIDGR
SARLYGVTAPAFLCAMVLAVCANNIGVIWVA LEATTVITAFITVGHKWTRTALEATWKY
VYCSVGIAVAFLGTVLLYRARDSGAAAAGALLAUDILAEHAGLIDPGVARLAGGLLL
IGYGAKAGLFPFHWALDAHSQAPAPVSALMSGVLLAVAFSVLIKLRPILDAYSGPAY
LRNGLLVVGLATLLVAVLMLTVTGDVKRMLAYSSMEHMGLIAIAAAAGTTLAIAAALLL
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YYLFLAGYPDRRVELEYVVPADNPEIRSLAYLSFPAGRFEREWADLYGIRPVGHPKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="wsnamsilvdpraagglvlasvlivwrrdlraivrllawggaal
Aaiplirgirdndraliavglavlalralvlpwllaravgaeaagreatplvwtass
llitagltltafaitqpvvnlepgvtinavpaafavylialfvwttklhavsqaagfl
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     /translation="MSYLAGAAQIGGVMVGAPLVIGMTRQVRARWEGRAGGLLQPWR
DLLKQLGKQOITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPLDPSADLFAVVG
LLFLGTVALTLAGIDTGTSFGGWGASETTIAALVEPTILLAVFALSIPAGSANLGAL
VASTIDHPGHVVSLAGVLAFVALVIVIVAETGRLPVDNPATHLELTWVHEAVVLEYAG
PRLAVVEWAGWRLTAVLALLANLFLPWGIAGAAPTALDVLTGVVAVAAKVAILAVLL
ATFEVFLAKLRLFRVPELLAGSFLLALLAVTAANFFTVGA"
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/gene="hycE"
/gene="hycE"
/note="Rv0087, (MTCY251.05), oxidoreductase, len:
492.hycE, similar to HYCE_ECOLI P16431 formate
hydrogenlyase subunit 5 (569 aa) FASTA scores, opt: 680,
z-score: 808.1, E(): 1.8e-38, (31.2% identity in 449 aa
overlap) and to NDD ECOLI P33600 nadh dehydrogenase i
chain d, (407 aa) FASTA scores.opt: 245, z-score: 293.1,
E(): 8.9e-10, (24.5% identity in 368aa overlap)"
                                                                                                                                                                                                                                                                 /gene="hycp"
/note="Rv0085, (MTCY251.03), len: 220. hycp, similar to
splp77524 HYFE_ECOLI HYDROGENASE-4 COMPONENT E (216
aa) FRASTA SCOTES: opt: 204 z-score: 272.1 E():1.2e-07;
25.5% identity in 216 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA98921.1"
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/db_xref="SWISS-PROT:Q10882"
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/db_xref="SPTREMBL:010884"
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/gene="hycP"
967. .1629
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(URL, http://www.sanger.ac.uk/Projects/M.tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M.tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old peen renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G i C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where pussible we choose an initiation codon initiation which is preceded by an upstream ribusome binding site sequence (optimally 5-1 Mp before the initiation codon). If this cannot be identified we choose the invast upstream
                                                                                               /note="RV3448, (MTCY77.20), len: 467 aa. Unknown membrane protein, contains PS00402 Binding-protein-dependent transport systems inner membrane comp signature. Some similarity to AL021930[MTV035_18 Mycobacterium tuberculosis (472 aa) fasta score, opt: 429 z-score: 4884 E(): 1.1e-19; 28.2%identity in 479 aa overlap" /rransl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Submitted on behalf of the Mycobacterium

Submitted (1.740-1998) Submitted on behalf of the Mycobacterium

submitted (1.740-1998) Submitted on behalf of the Mycobacterium

tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome

Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique

Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,

75724 Paris Cedex 15, France B-mail: parkhill@sanger.ac.uk

on Jun 27, 1998 this sequence version replaced gi:2104370.
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/Astrain="H37Rv"
/db_xref="taxon:8332"
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/db_xref="taxon:8332"
/clone="Y77"
                                                                Mycobacterium tuberculosis H37Rv. Mycobacterium tuberculosis H37Rv
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78. .164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv3448"
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                    GI:3261766
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Z95390 AL123456
Z95390.1 GI:32
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TITLE
JOURNAL
                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
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KEYWORDS
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AUTHORS
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                                                                             SOURCE
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probable precursor of serine protesse. Has putdive signal peptideat N-terminus and hydrophobic stretch at peptideat N-terminus three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 903863 SERINEPROTEASE (390 aa) opt: 241: E(): 8c-07; (38.0% identity in 387 aa overlap), similar to MTCX15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAALAYAVIVKNAV LVAAGORTGGAAQCPPOAPGYTKOSSYTVAVSPAAYDDYYLTVGS
VNAQABEISAFTLAGTAVIVAARGEAVTSLSPEGIGTYVNLAGGIGS LP LSGTSYAAPV
VSGLAALI KARET LLTAKOVMOR LESTAHHIPPAGWIPLVGNGTVDALAAVSSINSLPQA
GLATSIPALVAVETRESTEGESDERALIHTAPAGAALTLALAATLATASRRIRPGRN
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KUSSSKFAPVGDPSSTGVGDVDTMAKAVRTAADLGASVINISSIACVPAAAAPDDRAL
                                                                                                                                                                                                                                                                                                                                                /, journal of the control of the con
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                                                                                                                                                                                                                            GASPATAARYQI,SAI,GAPALPNATTLAQCGTRDGAVI,VLHKSSAQPPTPRCDDVAEAV
AAALDTTARPQCQRTTRLSGALAASCTTAGGGLMLVRNALGTNVTRYSDATAGVVAAA
GI,AALLFAVTACRTYRDP1AGLTLSVTATTFGAVAGI,LAVPGVHOVHSVI,VAAMAAAA
                                                                                                                                                                               /translation-"MPTSDPGLRRVTVHAGAQAVDLTLPAAVPVAT1.IPSIVDILGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1862. 1894
/gene-"Ry344y"
/note-"PS00137 Serine proteases, subtilase family,
histidine active site"
2456. 2488
/gene-"Ry3449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"PS00136 Serine proteases, subtilase family, aspartic acid active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Rv3449, (MTCY13E12.02), len: 455. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           611. >43401
/organism-"Mycobacterium tuberculosis H37Rv"
/strain-"H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start-i
/rransl_table-11
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/product="hypothetical protein Rv3448"
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complement(2810, .4222)
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1478. .284
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/yene-"Rv3449"
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1.SPLFGSRATILICHTPPLCHYGPGREFSGHIDDYILTYTTGAASFVVGRLRAGSVPH
LPGSVPQLFGSVLQMPGTAAPAPESLHGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPASAGCPDAEVVFARGTGEPPGLGRVGQAFVSSLRQQTNKSIGTYGVNYPANGDFL
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                                                                                                                                                                                                                                                                  Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., bodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Teischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

Location/Qualifiers
of 280 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MT3559"
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871. .1856
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/note="similar to SP:Q00298; identified by sequence
                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism~"Mycobacterium tuberculosis CDC1551'
                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 16384)
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section 246
Mycobacterium tuberculosis CDC1551,
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Mycobacterium tuberculosis CDC1551
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96. .839
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/gene="MT3560"
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                    complete genome.
AE007160 AE000516
AE007160.1 G1:138
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VVORPAEDSAQVLTAROM LUVATESGSPTVLLLYGGRRAVVDLADPAVWALRLGGRV
PHVVAQSLLNAVPERPRITAPRIRGGRASVGLPGFLVGGVVRITRASGDETVVVLED
GVQRIGQVAADLLRFGDSGGSVNVPTVAPDVIRVAPIVNTLPVSAFPDRFPTPVDGSP
                                                                                                                                                                                                                    GRÄVTTLCVTWTPAQPGAÄRVAFLAGSGPPVPLGGVPVTLAQADGRGPALDAVYLPPG
RSAYVAARSLSGGGTGTRYLVTDTGVRFAIHDDDVAHDLGLPTAAIPAPWPVLATLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLVLGGYSGGATVIDIVAGVPLGSISFGSPLPAAYADNVAAVAVFGNPSNRAGGSLSS
LSPLFGSKAIDLCNPTDPICHVGPGNEFSGHIDGYIPTYTTQAASFVVQRLRAGSVPH
LPGSVPQLPGSVLQMPGTAAPAPESLHGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //orde="R.Y3451, (WTCY13E12.04), len: 247. Function: probable cutinase, similar to several, contains cutinase, serine active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU 050664 probable cutinase cy339.08c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCY13E12.05 (FASTA score: E(): 0; (59.2% identity in 211 aa overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15964 ACGACCACACCCCGGTCATCGACACCCCCCGATGCGGCCGCCATCGACCGCGCCACCC 16023
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                                                                                                                                                                                                                                                                                                                    /gene="Rv3450c"
/note="R500013 Prokaryotic membrane lipoprotein lipid
attachment site.
complement(4228. .4231)
/note="possible RBS, GGAG, for Rv3450c"
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Pred. No. 2.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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/db_xref="G1:2104374".
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                                              /db_xref="SPTREMBL:006317"
                                                                                                                                                                                                                                                                                               complement(4049. .4081)
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complement(6706.7125)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPPAKKGPATSARKGOKTRREKKNVPHGAAHIKSTFNNTIVTI
TDPQGNVIAWASSGHVGFKGSRKSTPPAAQLAAENAARKAQDHGVKKVDVFVKGPGSG
RETAIRSLQAAGLEVGAISDVTPQPHNGVRPPKRRRV"
ARTESDLLDIRNFGQKSIDEVKIKLHQLGLSLKDSPPSFDPSEVAGYDVATGTWSTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to SP:P45810; identified by sequence
                                                                                                                                                                                             /note="similar to SP:P81288; identified by sequence
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Pred. No. 9.4e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(7129. .7503)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7719, .7832)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (7719. .7832)
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                                                                       complement(6092. .6697)
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                                                                                                                                                                                                                                   similarity; putative"
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/transl_table=11
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RIPVDSIYSPVLKVYXVDATRVEQRTPFDKLILDVETKNSISPRDALASAGKTLVEL
FGLARELNVEAEGIEIGPSPAEADHIASFALPIDDLDLTVRSYNCIKREGVHTVGELV
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INVTNAYSGSLAWTNSFTRLTKHYPGRVVFLGVNLAIALILMEANMFDFLNTILGCYA
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COMPLEMENT (3485. 4378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:J01685 SP:P02416 GB:X00766 PID:147716 PID:42800; identilied by sequence similarity; putative"
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                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930621 seqs, 428662619 residues
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 111. 112.:. 114.:. 115.:. 117.:. 119.:. 221::.

10:

SUMMARIES

	Description	M. tuberculosis ma	DNA for M. tubercu	Mycobacterium tube	M. tuberculosis ce	DNA for M. tubercu	BCG deletion regio	C glutamicum codin	Corynebacterium gl	Bordetella pertuss	plasmid prrpl-35 D	Sequence including
	ID	7 AAT33658	9 AAV18649	5 AAQ89200	7 AAT33656	9 AAV18647	7 AAT33537	2 AAH65816	2 AAF71958	1 AAA64886	AAN50261	0 AAN90631
	gth DB	650 17	650 19	535 16	535 17	535 19	12412 17	413 23	413 23	536 2	853 6	1853 10
æ	Query Match Length DB ID											4.0
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	12	18	4.0	8051	18	AAT72685	Sugar biosynthesis
	13	9 0	0.4		7 5	AAXZ3774 AAA64890	Bordetella pertuss
U	14	φ α		~	2.7	AAH68526	C qlutamicum codin
	16	17	2	5	7	AAC98508	Human colon cancer
	17	17	3.8		50	AAX98072	Nucleotide sequenc
ပ	18	17	3.8		20	AAX98073	Nucleotide sequenc
ပ	19	17	æ.;		22	AAI 104/3	Drobe #400 101 gen
O (	20	17	x x		77	AA131727	Probe #413 used to
υ c	2.7	17	0 00		2.5	AA119727	Probe #9660 for ge
ט נ	23	17			22	AA144923	Probe #13609 used
0	24	17	3.8		20	AAX98044	Nucleotide sequenc
	25	17	æ. ~		13	AAQ20926	C10-E15 DNA Fragme
	26	17	٠. م		E 0	AAQ20923	Niclestide seguenc
	27	17	m :		2:0	AAX98046	Psudomonas sp ABC
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ر:	30	17	0 8		17	AAT09251	SCK phosphotyrosin
ر	3.5	17	. ~		20	AAX98068	Nucleotide sequenc
)	32	17	3.8		15	AAQ56930	Bacillus thuringie
	33	17	æ ~		2.5	AA159617	Human polynucieoti
O	34	17	ж		77	AAFBUBSS	pseudomonia a presentation de serviciones de de s
	35	17	×. ^		77	AAF 26409	Microbispora therm
	36	1,	o a			AAH65828	C qlutamicum codin
	. 8	17	38.		20	AAX98041	Nucleotide sequenc
	36	17	3.8		22	AA157831	Human polynucleoti
ပ	40	17	3.8		2.5	AA157831	Human polynucleour
U	41	17	დ (		22	AADU/U24	pimaricin biosynth
	2 7	17	ب ر ص م		77	AAF 24691 AAF 63074	IdG-Fc binding pro
	4 4 7 4	17			20	AAX98035	sotide seque
υ	45	17	. 60		20	AAX98035	Nucleotide sequenc
						A1.1GNMENTS	
RES	RESULT 1						
ID	AAT33658		standard;	d; DNA;	059	ВР.	
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X X :	passive	-	immunisat	: i	dene t	herapy; ds.	
X X SO	Σ	cobacterium		tuberculosi	S	strain H37Ra (ATCC 2	25177).
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X C	53	-AUG-1996.					
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PF	20-FEB	B-1996;	9	16WO-US0215	2155		
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DR DR	WPI; P-PS	1996-425086/4 DB; AAW02303.	25086 )2303	5/42.			
×				•			-
PT	DNA and	ving Surv	ve.	tuberculosis within macro	osis nacro teri	uberculosis ability to enter man within macrophage(s), useful in wormbarterium tuberculosis info	nmallan c vaccines ection
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                                                                                                                                                       176;
                                                                                      occurrence
                                                                                                                                                                                                                                                                                                                                         AAQ89200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riley LW;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                               Best Local
                                                                                                                                                       Matches
                                                                                                                                                                                                                338
                                                                                                                                                                                                                                                                                                             AAQ89200
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                                                                                                                                                                                                                                                     A DNA molecule (AAT3358) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT3355) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cellinvasive clones. It can be incorporated into a vector and used for prodn. of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule tuberculosis the ability to enter mammalian cells.
                                                                                                                                                                                                                Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                       cgcgggccacctttgaagccgtgctagccaaactggccgcccccggcggcgaccaaccccg 337
                                                                                                                                                                                                                                           acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                               38.9%; Score 176; DB 17; Length 650; 100.0%; Pred. No. 4.6e-77; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                    Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular uptake protein; vaccine; infection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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 Claim 7; Page 45; 67pp; English
                                                                                                                                                                                                                                                                                                                                                  ВР
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                                                                                                                                                                                                                                                                                                                                                  AAV18649 standard; DNA; 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                   Conservative
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/*tag=
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                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                  Matches 176;
                                                                                                                                                                                                                                                                                                                                                                     AAV18649;
                                                                                                                                                                 Query Match
                                                                                                                                                                                                       278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acgaccacacceccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibudies raised against it can be used to treat mammals already exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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                                                                                                                                                                                                                                                                                                                                     Length 650;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                             Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                        Score 176; DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                     38.9%; ; 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; tuberculosis; ss.
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A DNA molecule (AAT33656) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The enter macrophages and to survive within macrophages. It is sequence is given in AAM02301. The DNA was obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cell-invasive clones. The DNA includes 2 separate coding regions (see also ART33657-58) coding for the cell entry (AAM02302) and macrophage survival (AAM02303) proteins. It can be used to produce the cellular uptake proteins used as vaccines or to facilitate uptake of other
                                                                                                                        Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                    materials, e.g. therapeutic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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P-PSDB; AAW47541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chong P, Riley LW;
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    macrophages. It encodes a polypeptide having a mol. wt. of about 50°55 kDa, pref. 52 kDa. The AA sequence represents a highly hydropholic perion at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
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0
                                                                                                                                                                                                                                                                                                                                                                                                                     cell entry; macrophage; passive immunisation;
                                                                                                                 DB 16; Length 1535; 4.3e-77;
                                                                                                                                        Indels
                                                                                Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= macrophage survival protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
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/label= ORF-1
/product= cell entry protein
886..1535
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                                                                                                                 Query Match
38.9%; Score 176; DB
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 17f; Conservative 0; Mismatches
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/label= ORF-2
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                                                                             cgcgggccacttltqaagccgtgctayccaactggccgccccgggggggaccaaccccq 337
                                                                                                                                                          acgaccacaccequicategacaccacecegatgeggeegeeategaeegegaeaece 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an
                                                                                                                                                                                                                                          0;
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Length 1535;
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                                        Indels
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Score 176; DB 17;
Pred. No. 4.3e-77;
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/mie-"stop codon not given"
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                                          Mismatches
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  Query Match 38.9%; Scc
Best Local Similarity 100.0%; Pr
Matches 176; Conservative 0;
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AAH65816;
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                                                                                                                                               This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region results in an avirulbance phenotype of the mycobacterium. 2 other deletion regions (see AAT33535 and AAT33536) have also been detected. Identification involved screening a BCG cosmid library with a
                                                                                                                             Gaps
ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                           Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                                                                                                                                                                          BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
                                                                                                                              ;
0
                                                                                                          Length 1535;
                                                                                                                              Indels
                                                                            Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "BCG delta ] deletion region"
                                                                                                         38.9%; Score 176; DB 19;
100.0%; Pred. No. 4.3e-77;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        BCG deletion region 3 and flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1406..10673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis strain BCG
                                                                                                                                                                                                                                                                                                standard; DNA; 12412
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                                                                                                                                Conservative
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                                                                                                                      Similarity
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                                                                                                                        Best Local Sir
Matches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acgaccacaccenggicalegacaeracceeegalgeegeegeealegacegegacaeee 397
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radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of presence or absence of deletion junctions (see AAT33538-46), or by detecting the presence or absence or absence or absence of the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176; DB 17;
Pred. No. 3.7e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%; SCC.
100.0%; Pre
0; 1
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2000JP-0159162.
2000JP-0280988.
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176; Conser
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Tateishi N,
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are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lygine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum MP protein nucleotide sequence SEQ 1D NO:411
                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                           Gaps
                                                                                                                                                                          0;
                                                                                                                                                       22; Length 1413;
                                                                                                                                                                           0; Indels
                                                                                                                         Seguence 1413 BP; 259 A; 350 C; 395 G; 409 T; 0 other;
                                                                                                                                                       DB 2
17;
                                                                                                                                                                            Mismatches
                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                4.0%; Scc-
100.0%; Pred
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99DE-1031478.
99DE-1031510.
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99DE-1031634.
99DE-1031636.
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99DE-1030476.
99US-0142101.
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99DE-1031418.
99DE-1031419.
99DE-1031420.
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99DE-1031573.
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99DE-1031428.
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99DE-1031435.
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                                                                                                                                                                    Best Local Similarity 100.
Matches 18; Conservative
                                                                                                         European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200100843-A2.
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08-70L-1999;
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AAF71753 to AAF7.230 encode the Corpuebacterium qlutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aroundic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
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Pred. No. 17;
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100.0%; Pred
0; F
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990E-1042129.
20000S-0187970.
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99DE-1040766.
99DE-1040832.
99DE-1041378.
99DE-1041379.
99DE-1032228.
99DE-1032229.
99DE-1032230.
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99US-0148613.
99DE-1040764.
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Matches 18; Conservative
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                                                                                                                          14-JUL-1999;
14-JUL-1999;
12-AUG-1999;
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31-AUG-1999;
31-AUG-1999;
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31-AUG-1999;
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03-SEP-1999;
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03-SEP-1999;
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28-JUN-1983;
28-JUN-1983;
14-JUN-1984;
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28-JUN-1983;
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                                                                                                                                           30-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                         (vitamin C)
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promoter
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  promoter
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                                                                                                                                                                                                                                                                                                                                          Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at host cells. The present sequence is a coding sequence of B. pertussis. No name has been specified for the present sequence. The present sequence may be a housekeeping gene. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The present sequence is located within a pathogenicity island (see AAA64890) which also carries, a number of genes encoding proteins involved in the type III secretion system of B. pertussis. See AAA64849. And ABA111-B14146 for details of the coding sequences and proteins identified in the pathogenicity island, of the present invention.
                                                Type III secretion system; virulence factor; pathogenicity island; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pTrp1-35 DNA encoding the 2,5-diketogluconate-reductase yene.
                                                                                                                                                                                                                                                                                           Novel polypeptides derived from Bordetella pertussis, useful for treating and diagnosing Bordetella infection -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 18; DB 21; Length 1536; 100.0%; Pred. No. 17; tive 0; Mismatches 0; Indels
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                             Bordetella pertussis coding sequence # 2.
                                                                                                                                                                                                                                                                                                                         Example 2; Pages 154-156; 165pp; English.
                                                                                                             /*tag= a
/product= "Protein # 2"
                                                                                       Location/Qualifiers
1..1536
/*tag= a
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                                                                                                                                                                                                    98GB-0028217.
                                                                                                                                                                                 99WO-EP10297.
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       02-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 18; Conservative
                                                                     Bordetella pertussis.
                                                                                                                                                                                                                                                               WP:; 2000-452178/39.
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                                                                                                                                         WO200037493-A2
                                                                                                                                                                                21-DE(:-1999;
                                                                                                                                                                                                     21-DEC-1998;
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Sequence including 2,5-diketogluconic acid reductase gene and purpl35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller JV;
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100.0%; cred, No. Fe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1853 BP; 327 A; 645 C; 587 G; 294 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasteter WH, Lazarus RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pure 2,5 di:kvto-gluconic acid reductase - precombinant DNA methods for assorbic acid prodn.
                                                                                                                                                         /*tag= d
/!abel- 2,5-DKG-reductase gene
                    coli trp promoter
                                                                             coli trp promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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229..234
/*Lag≈ a
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                                                                                                                                                                                                                                                                                                                               84US-0620585.
83US-0508409.
83US-0508410.
83US-0508628.
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84US-0620652.
                                                       /*tag= b
/label= E.
279..283
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/*tag= a
/label= E.
252..257
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296..1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENEN'FECH INC
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Best Local Similarity
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2 Polynucleotides (AAT72684 and AAT72685) represent 2 distinct clusters of genes encoding enzymes (AAW19734-36 and AAW19737-42) involved in sugar biosynthesis and attachment in Saccharopolyspora erythraea. The eryB genes are involved in the biosynthesis of L-mycarose and the eryC genes involved in the biosynthesis of D-desosamine. Worel glycosylation-modified polyketides are produced by selectively altering, inactivating or augmenting these eryB and/or eryC genes and introducing them into polyketide-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene cluster; bacterium; enzyme; macrolide; antibiotic; erythromycin; secondary metabolite; eryBII; eryCIII; eryCII; hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes involved in sugar biosynthesis and attachment - used tgenerate polyketide antimicrobials etc. with altered pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.erythraea erythromycin-synthesis gene cluster eryAI-eryK.
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                                                                                                                                                                                                                                                                                                                                                                                                       Summers RG;
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           /label= eryBV
2348..3061
/*tag= c
/label= eryCVI
3214..4677
                                                                                     /*tag- d
/label- eryBVI
4674..5879
                                                                                                                             /*tag= e
/!abel= eryClV
5917..7386
                                                                                                                                                                                                                  /*tag= g
/label= eryBVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 4B; 85pp; English.
 b
eryBV
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/label- eryCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-351066/32.
P-PSDB; AAW19737-42.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycosylation
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                                                                                                                                                                                                                                                                                                                  23-DEC-1996;
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ID AAX2
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AC AAX2
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KW Gene
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See also AAN94347 and AAN94348.
                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant prodn. of 2,5-diketogluconic acid reductase - useful for converting 2,5-DKG stereoselectively into 2-ketogluconic acid, a precursor of vitamin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyketide, glycosylation, eryBIV; eryBV; eryCVI; eryBVI; eryCIV; erCV; eryBVII; L-mycarose, D-desosamine; antimicrobial; antibiotic; antifungal; fungicide; anticancer; cytostatic; anthelmintic; ss.
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0
'label=E. coli Trp promoter
                                            promoter
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/product=2,5-DKG reductase
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00.0%; Pred. No.
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                            /*tag= b
/label=E.coli Trp
279..282
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/label= eryBIV
1048..2295
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83US-0508409.
83US-0508410.
84US-0620651.
84US-0620652.
84US-0620585.
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                                                                       /*tag= c
296..1129
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Best Local Similarity 100.(
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                ..257
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                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
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28-JUN-1983;
28-JUN-1983;
14-JUN-1984;
14-JUN-1984;
14-JUN-1984;
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                                                                                                                                                                         08-MAR-1989
                                                                                     mat_peptide
                                                                                                                                            EP305608-A.
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                 promoter
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ID AAT7
                                                           RBS
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02-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                           gene= "eryBVI"
|product= "dTDP-4-keto-L-6-deoxyhexose-2,3-dehydratase"
|837..604
                                                                                                                                                                                                                                                                                      /gene= "eryBVII"
/product= "dTDP-4-keto-D-6-deoxyhexose-3,5-epimerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences encoding enzymes involved in macrolide biosynthesis – useful for producing hybrid secondary metabolites, particularly erythromycin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene= "erycv"
/gene= "erycv"
/product= "dTDP-D-4,6-dideoxyhexose-3,4-reductase"
                                                                                                                                         /gene= "eryBIV"
/product= "dTDP-keto-L-6-deoxyhexose-4-reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene= "eryGIV"
/product= "dTDP-D-6-deoxyhexose-3,4-dehydratase"
6/80..7549
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                                                                                                                                                                                                                         /gene= "eryBV"
/product= "mycarosyltransferase"
2510..323
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Fromentin C, Mendez C, Salas J
   glycosylation; macrolactone; oleandomycin; ds.
                                                                          Socation/Qualifiers
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/label= ORF18
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/label= ORF17
                                                                                                          /*tag= a
/label= ORF13
                                                                                                                                                                                                          /label= ORF14
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97FR-0009458.
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                                       Saccharopolyspora erythraea
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cluster is shown in AAX25772. The genes are used to produce hybrid secondary metabolites in S.erythraea, i.e. erythromycin analogues which may have improved properties or as hybridisation probes for isolating homologous genes involved in glycosylation of macrolactones in macrolide-producing strains (specifically oleandomycin-producing strains of Streptomyces antibioticus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial infection; anti-bacterial; vaccine; whooping cough; type III secretion system; virulence factor; pathogenicity island; ss.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         ;;
0
                                                                                                                                                                                         Score 18; DB 20; Length 8160;
Pred. No. 15;
Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis pathogenicity island coding sequence.
                                                                                                                                      Sequence 8160 BP; 1259 A; 2927 C; 2789 G; 1185 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*!ag= a
/product= "Protein # 1 (AAB14147)"
complement (2055..3590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protein # 4 (AAB14150)"
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complement (11906..13003)
/*tag= m
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complement (11532..11909)
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complement (10752..11120)
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100.0%; FIS
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Matches 18; Conserv
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P-PSDB: AABI4111, AAB14112, AAB14113, AAB14114, AAB14115, AAB14116, AAB141117, AAB14118, AAB14119, AAB14121, AAB14122, AAB14123, AAB141213, AAB14129, AAB14129, AAB14129, AAB14130, AAB14131, AAB14132, AAB14132, AAB14133, AAB14134, AAB14135, AAB14136, AAB14137, AAB14137, AAB14137, AAB14137, AAB14137, AAB14137, AAB14137, AAB14140, AAB14140, AAB141414, AAB14142, AAB14143, AAB14151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at host cells. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The present sequence is a pathogenicity island from B. pertussis. The present sequence encodes a number of proteins involved in the type III secretion system of B. pertussis i.e. Bordetella pathogenicity protein. The proteins encoded by the present sequence may be used to treat or diagnose B. pertussis infection, e.g. as a vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides derived from Mordetella pertussis, useful for treating and diagnosing Bordetella infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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                                                                                                                                                                              /product= "Protein # 5 (AAB14151)"
               /*tag= al
/product= "Orf13 (AAB14144)"
complement (31773..33005)
                                                               am
t= "Orf14 (AAB14145)"
                                                                                                                              /product= "Orf15 (AAB14146)"
complement (33002..34852)
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                                                                              /product= "Or
32370..33014
                                                                                                                                                                                                                                                                                                                                              (ULBR ) UNIV LIBRE BRUXELLES.
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Matches 18; Conservative
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                                                                                                                                                                                                             WO200037493-A2.
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The present invention provides a number of nucleotide and protein are dequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analyshing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing main o acids, nucleic acids, vitamins, saccharides and organic acids, notes the present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                       Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 349980 BP; 79274 A; 90638 C; 98727 G; 81341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO: 7061; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                            16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                       18-DEC-2000; 2000EP-0127688
Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-376931/40.
                                    EP1108790-A2
                                                                                                                                                                                                                                                                                       Nakagawa S,
Tateishi N,
                                                                              20-JUN-2001
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Query Match
4.0%; Score 18; DB 22; Length 349980;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; 214 teacettgageaaceage 231 Matches ŏ

Search completed: April 3, 2002, 02:03:22 Job time: 3311 sec

0;

Gaps

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Sequence 5, Application US/08464052
Sequence 5, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                 Sequence 5, Applisequence 35, Applesequence 35, Applesequence 3, Applisequence 3, Applisequence 3, Applisequence 1, Applisequence 1, Applibatent No. 5240849
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Sequence 1, A
Patent No. 524
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Sequence 13,
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Pred. No. 1.2e-74;
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ER: 19603/185 (D-1485B)
                 PCT US91 06234A-5
US-08-646-590B-35
US-09-412-184-35
5240B49-4
US-09-124-541-3
US-08-124-79B-3
US-08-124-981A-1
US-09-037-192-45
US-09-037-192-45
US-09-037-143-45
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US-09-037-143-45
US-09-037-144-45
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100.0%; Pred. No. ...
0; Mismatches
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US-08-588-976-13
US-09-248-335-63
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APPLICATION NUMBER: US/08/464,052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-464-052-5
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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nucleic acid
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MEDIUM TYPE: Floppy
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Best Local Similarity
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US-08-464-052-5
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Sequence 1, Appli
Sequence 2, Appli
                                                                                                                                                                     April 3, 2002, 00:40:06; Search time 89.67 Seconds (without alignments) 1144.134 Million cell updates/sec
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Sequence 15,
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Sequence 8
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Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US44-09863-1

US-08-689-411-1

PCT-US44-09863-1

US-08-103-84-0A-1

US-09-103-84-0A-1

US-09-103-84-0A-1

US-09-103-84-0A-1

US-09-103-84-0A-1

US-09-103-84-0A-1

US-08-08-09-1

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US-08-08-09-1

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US-08-353-550-5

US-08-353-550-5

US-08-353-550-5

US-08-353-550-7

US-08-31-409-1

US-08-198-1

US-08-198-1

US-08-198-1

US-08-103-440-1

US-08-103-440-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
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Match Length
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Maximum DB
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                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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338 acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELEPAN: (716) 263-1304
TELEPAN: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 Dasse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANEBDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.9%; Score 176; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 176; Conservative 0; Mismatches
                                                                                                                                                                               Sequence 5, Application US/08461002
Patent No. 6214543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08689411
Patent No. 6224881
GENERAL INFORMATION:
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US-08-461-002-5
                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOP( LOGY: unknown
                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
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US-08-461-002-5
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US-08-689-411-5
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APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
FILLIG DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 176; DB 4; I larity 100.0%; Pred. No. 1.2e-74; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                     dinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman, Michaell.
REGISTRATION NUMBER: 30,727
REFERENCE/FOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08464052
; Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
Riley M.D., Lee W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: double unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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Best Local Similarity
Matches 176; Conserv
                                                                                                                                                      STREET: Clinton
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                   U.S.A.
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COUNTRY: U.S.A.
ZIP: 14603
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                                                                                                                                                                                                                 COUNTRY: U
ZIP: 14603
                                                                                                                                     ADDRESSEE:
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TELEFAX: (716) 263-1600
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TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 acgaecacaccecggtcatcgacaccaccecgatgeggecgecategaecqcqacacce 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1535;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.9%; Score 176; DB 3; I
100.0%; Pred. No. 1.1e-74;
Live 0; Mismatches 0;
                                                                                                                                                                            NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOSKET NUMBER: 19603/186 (D-1485H)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08461002 Patent No. 6214543 GENERAL IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                     FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-461-002-1
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CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
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                                                                                                                                                                                                                  Length 1535;
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kiley M.D., Lee W.
APPLICANT: Choug, Pele
APPLICANT: Choug, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUB
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Harqrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                              38.9%; Score 176; DB 4; 100.0%; Prod. No. 1.1e-74; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: LHM 10° Compatible
OPERATING SYSTEM: PC DOSZMS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-689-411-1
; Sequence 1, Application US/08689411
; Patent No. 6224881
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                                                                                                      TOPOLOGY: unknown; MOLECULE TYPE; DNA (qenomic)
US-08-461-002-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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TELEFAX: (716) 263-1600
INFORMATION FOR SED 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATFORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
             SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
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                                                                                                                                                                                                                                                           Matches 176; Conservative
INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
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                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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Length 1535;

DB 4;

Score 176;

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USA
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                                               US-08-390-878-18
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                                                                         1106 CGCGGGCCACCTTTGAAGCCGTGCTAGCCAAACTGGCCGCCCCGGCGCGACCAACCCCG 1165
                                                                                                                                    11166 ACGACCACCCGGTCATCGACACCCCCGATGCGGCCGCCATCGACCGCGACACCC 1225
                                                       278 cgcgggccacctttgaagccgtgctagccaaactggccgcccccggcgaccaaccccg 337
                                                                                                                  338 acgaccacacccggtcatcgacaccacccgatgcggccgccatcgaccgcgacacc 397
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                                Gaps
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                                                                                                                                                                                                                                                                      PCT-US94-09863-1

Sequence 1, Application PC/TUS9409863

GENERAL INFORMATION:

APPLICANT: Riley, Lee W.

TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR

TITLE INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
             Pred. No. 1.1e-74; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMUNICATION INFORMATION:
TELEPHONE: (716,263-1000
TELLEFAX: (716)-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%; Score 176; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08; Pred....
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy-disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Micha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 38.9%
Best Local Similarity 100.0
Matches 176; Conservative
         Best Local Similarity 100.
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Clincon
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14603
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GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: HITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UUBERCLUGSIS

FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 gcagccaaqcccaacgcaaccacqacqqctggccgggctgcgcgcgcgctgatc 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
WUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townscad Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12412;
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 9.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,498
ER: 15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 18, Application US/08390878
; Patent No. 5700683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLONNOL, TOOK
NAME: Hunter, Took
REGIGTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 12412 base pairs
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ATTORNEY/AGENT INFURMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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Best Local Similarity
Matches 176; Conserv
                                      GENERAL INFORMATION:
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INFORMATION:
       Patent No. 5998194
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| Patent No. 6294328
| GENERAL INFORMATION:
| APPLICANT: FLEISCHMAN, Robert D.
| APPLICANT: FLEISCHMAN, Robert D.
| APPLICANT: FRASER, Claire M.
| APPLICANT: FRASER, Claire M.
| APPLICANT: FRASER, Claire M.
| APPLICANT: PRASER, Claire M.
| APPLICANT: PRASER, Claire M.
| APPLICANT: PRASER, Claire M.
| TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM ITLE OF INVENTION: DNA SEQUENCES
| TITLE OF INVENTION: TUBERCULOSIS |
| FILE REFERENCE: 24566-22007.00 |
| CURRENT APPLICATION NUMBER: US/09/103,840A |
| CURRENT FILING DATE: 1998-06-24 |
| NUMBER OF SEQ ID NOS: 2 |
| SOFTWARE: Patentin Ver: 2.1 |
| SEQ ID NO 1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 cgcgggccacctttgaagccgtgctagccaaactggccgccccggcggcgaccaacccg 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccqcgacaccc 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%; Score 176; DB 4; Length 4411529; 100.0%; Pred. No. 5.8e-75; Live 0; Mismatches 0; Indels 0;
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1.2;
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILIN: DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                      TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-08-576-626A-2
: Sequence 2, Application US/08576626A
                                                                                                                                                                                                                                                                             Query Match 38.9
Best Local Similarity 100.
Matches 176; Conservative
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US-09-103-840A-1
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APPLICANT: Hideya FUJIWOTO, Kimiko ITOH
APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDERS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 3.50 inch, 144 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.0%; Score 18;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEPHOXE: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASLSKO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/07982712
Patent No. 5436391
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Computible OPERATING SYSTEM: DOS SOFTWARE: FastSKQ Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8051 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
APPLICATION NUMBER:
FILING DATE:
ATTORNEY:
                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEU ID NO:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                              STREET: 100 Abbott
CLTY: Abbott Park
STATE: 111inois
                                                                                                                                                                                                                                                                              60064 - 3500
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                                                                                                                                                                                                                                                             COUNTRY: USA
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                 Query Match 3.8'
Best Local Similarity 100.
Matches 17; Conservative
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MEDIUM TYPE: Diskett
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Matches 17; Conserv
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                                                                                                                                                                                                                            US-08-449-093A-18
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Patent No. 5641654
GENERAL INFORMATION:
APPLICANT: No. 5641654cru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: No. 5641654cru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%; Score 17; DB 1; Length 42;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,3.50inch,1.4Mb storage COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COPERATING SYSTEM: Macintosh Classic
SOFTWARE: Macrosoft Word Version 4.0A
CURRENT APPLICATION DATA:
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FILING DATE: June 22, 1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 18:
                                                                  19921127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: other nucleic acid US-07-982-712-4
COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WORDER-FECT 5.1 CURRENT APPLICATION UNMERR: US/07/91 FILING DATE: 19921127 CLASSIFICATION: 800 PRIOR APPLICATION UNMER: FILING DATE: FILING DATE: FILING DATE:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 gactggctacaccccga. 173
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LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 42 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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CITY: Boston
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Sequence 15, Application US/08081072

Sequence 15, Application US/08081072

Sequence 10, 2641654

APPLICANT: No. 5641654oru MAKI, Kenjiro YANAGUCHI, Ayumi APPLICANT: TOYOSHIMA, and Michinori KOHARA

TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC

TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
                                                                                                                                                                                                                                                                              Sequence 18, Application US/08449093A
Patent No. 5662906
GENERAL INFORMATION:
APPLICANT: NO. 5662906oru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: NO. 5662906oru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: NOVOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-8 HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND 17S USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
Score 17; DB 1; Length 742;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACUNESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
STRY: Boston
STATE: Massart.
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OURENT APPLICATION SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,093A FILING DATE: May 24, 1995
CLASSIFICATION: 124
PRIOR APPLICATION 1942
PRIOR APPLICATION 1948: 08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 07/726,141
FILING DATE: July 8, 1991
CLASSIFICATION: 424
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to genomic RNA
US-08-449-093A-18
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TITLE OF INVENTION: DIAGNOSIS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
STREET: 130 Water Street
CITY. Boston Date, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston Date, Bronstein
STATE: Massachusetts
COUNTRY: Uses
COUNTRY: Use, Broincoh Lassic
CONFORTE: Radable FORM:
MEDIUM TYPE: Floppy Disk, 3.50inch, 1.4Mb storage
COMPUTER: Radable FORM:
MEDIUM TYPE: Floppy Disk, 3.50inch, 1.4Mb storage
COMPUTER: Apple Macintosh Classic
COMPUTER: Apple Macintosh Classic
COMPUTER: Apple Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
CURRENT APPLICATION NUMBER: 22, 1993
CLASSIFICATION NUMBER: 22, 1993
CLASSIFICATION NUMBER: 22, 1993
CLASSIFICATION NUMBER: 22, 1993
CLASSIFICATION OF SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE TYPE: CONDITION: 15:
MOLECULE TYPE: CDN A to genomic RNA
US-08-081-072-15

Dest Local Similarity 100 0%; Pred: No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 231 caatacgacggcatgtc 247
DD 424 CAMTACGACGGCATGTC 440
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Search completed: April 3, 2002, 03:06:30 Job time: 8784 sec

Perfect score:

Sequence:

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BEB850262 uw15a09.9
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BFB9683349 kCl-CT024
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Notact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: capabs.remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

High quality sequence slop: 739.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       BG285414 1100 bp mRNA EST 21-FEB-2001
602409782F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4539236 5',
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//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism="IMAGE:4539236"
//Clone="IMAGE:4539236"
//Lissue_type="adenocarcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
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BG810322
AG699432
BF268065
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CNS0128P
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BF026228
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CNS011WW
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AQ398116
AA654704
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CNS01x7V
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AUTHORS
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BE499331 WHE0973_F
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BE416425 WIG008.E1
AA94237 LD28056.5
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A1518445 LD28056.5
                                                                           April 2, 2002, 22:46:21; Search time 1557.61 Seconds (without alignments) 3125.197 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1 (bases I to 458)

1 (bases I to 458)

1 (bases I to 458)

Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          БF924264 458 bp mKNA EST 19-JAN-2001
RC2-NT0225-271100-011-h09 NT0225 Homo sapiens CDNA, mRNA sequence.
BF9242844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                             Mismatches
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Pred. No.
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                             Pred.
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                                                                                                                                                                      157 CCGCTACGCCCAGCGGGTC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 c
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                                                             19; Conservative
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Matches 19; Conserv
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Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: Xhoī; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total kNA, and poly(A) RNA were prepared, a cDNA library was made, and the CDNA clones were in vivo excised to give pbluescript phagemids in the TJ close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                     /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF202807 454 bp mRNA EST 06-NOV-2000 WHEI784_H02_0042S Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHEI784_H02_004, mRNA sequence.
BF202807.1 GI:11117549
                                                                                                                                                                                                                                                                                                                                                                                                                  Caps
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
cap primer: Stratagene SK primer.
Location/Qualifiers
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/organism="Triticum destivum"
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/clone="WHE1784_H02_004"
/clone="WHE1784_H02_004"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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                                                                                                                                                                                                                                                                                                                                         DB 11; Length 1100;
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Gaps
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DB 11; Length 458;
69;
               Indels
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0
               Mismatches
                                                                          AQ573457
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DB 11; Length 454;

4.2%; Score 19;

Query Match

.; 0

GSS

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

DEFINITION

ACCESSION

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Unpublished (2000)
Unpublished (2000)
Unpublished (2000)
Us Department of Agriculture, Agriculture Research Service, Pacific Wost Area, Western Regional Research Center
BOO Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
1 (bases I to 525)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes: Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmprattenga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phiod quality 16. The threshold for highest quality sequence
                                                                                          Sorghum bicolor
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SpermaLophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                               The University of Georgia
Plant Schences Huilding, Rm. 2502, Athens, GA 30602-7271, USA
TTEL: 706 542 1865
Fax: 706 542 1805
                                                                                                                                                                                                                     and Pratt, L.H.
                                                                                                                                                                                             (bases 1 to 494)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L. An Esy database from Sorghum: light-grown seedlings Unpublished (2000)
On Jan 6, 2000 this sequence version replaced gi:6677590.
Contact: Cordonnier-Pratt MM
Department of Botany
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Pred. No. 69;
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High quality sequence stop: 401
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                GI:6859737
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Best Local Similarity 100.
Matches 19; Conservative
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/clone_lb="coli DH108"
/tissue_type="Leaf"
/note="Wetcor: pBeloBAC11; Site_1: HindIII: Site_2:
HindIII; Rice is one of two most popular grains in the
world Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n-24) with a happioid genome equivalent of 4% Mpp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
arbidopsis, makes it suitable for genomic studies. In
Arabidopsis, makes it suitable for genome constructed a BAC
library from oryza sativa, Nipponbare arivity. The
library contains 36,864 clones with an average insert size
of 1285 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9%. Two high density litters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
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                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
AQS73457 477 bp DNA GSS 02-JUN-1999 nbxb0081E24r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0081E24r, DNA sequence.
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                                                                                                                                                                                                                                                                                                          1 (bases 1 to 477)
Wing, R.A. and Dean, R.A.
Whollshed Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
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69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 19; DB 100.0%; Pred. No. 69; Live 0; Mismatches
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Location/Qualifiers
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                                                                                                                           AQ573457.1 GI:4973546
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AW287746
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source

FEATURES

Query Match

BASE COUNT

DEFINITION AW287746/c

RESULT

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Gaps

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traccheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Tri
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Fax: 5105595818
Email: oandersn@pw.usda.gov
Se.juence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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4.2%; Score 19; DB 10; Length 525;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels
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/tissue_inp_wiear_cold_stressed seedling cDNA library"
/tissue_inp_wiear_cold_stressed seedling classe_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/lab_host="E. coll SOLR"
/note="Vector: Lambda Uni 2AP XR, excised phagemid;
/germinated and grown aseptically in the dark at room
remperature on filter paper with water, nystutin and
cefotaxime in covered crystallization dishes. Five-day
old seedlings were transferred to 5 c cold room and kept
for 48 hr. The tissue, total RNA, and poly(A) kNA were
prepared, a cDNA library was made, and the CDNA clones
were in vivo excised to give pBluescript phagemids in the
full close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
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/organism="Norin 26"
/db_xref="Laxon:4565"
/dl_xref="Laxon:4565"
/clone="MuG008 E009"
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/clone=lib="TEC MUG Wheat Spikelet Library"
/clone=lib="TEC MUG Spikelet Library"
/clone=lib="Tec Mug Spikelets"
/clone=lib="Tec Mug Spikelets"
/clone=lib="Tec Mug Spikelets"
/cloue="Yector: pBluescript SK(-); Site_l: EcoRI; Site_2:
/cloue="Yector: pBluescript SK(-); Site_l: EcoRI; Site_2: EcoRI; Sit
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MUGGO08.E09R990628 ITEC MUG Wheat Spikelet Library Triticum aestivum
CDNA clone MUGGO8.E09, mRNA sequence.
/clone="WHE0364_A04_A08"
/clone_lib="Wheat cold stressed seedling cDNA library"
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International Triticeae EST Cooperative (ITEC)
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100.0%; Pred. No.
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Location/Qualifiers
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BE416425.1 GI:9414271
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Contact: Stapleton, M. BDGP
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Contact: Stapleton, M.
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gr used: 1.2 Kbp average
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bepermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 581)
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/tissue_type="Young spikelets"
/dev_stage="Feekes' scale 6-7"
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                                                                                                                       10; Length 575
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                                  4 others
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/organism="Triticum aestivum"
/cultivar="Norin 26"
/db_xref="taxon:4565"
/clone="MuG008.E10"
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100.0%; Pred. No.
tive 0; Mismatci
                                                                                                                          Score 19;
Pred. No.
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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BE416426.1 GI:9414272
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/clone="LD28056"
/clone="LD28056"
/clone="LD-"LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/dev_stage="X11 Hiue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
Xhol; Sized Iractionated cDNAs were directly ligated into
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Noptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 598)

5tapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson

5t., Consalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,

Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,

Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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                                                                                                                                                                 fruit fly.

Drosophila melanogaster

Brusophila melanogaster

Brusophila melanogaster

Brusophila melanogaster

Brusophila melanogaster

Brachycera;

Muscomorpha: Bephydroidea; Drosophilaidee; Drosophila.

| (bases 1 to 583)

Harvey, D., Brosstein, P., Hong, L., Evans-Holm, M., Su, C., Tsand, G., Lewis, S. and Rubhin, G.M.

BDGP/HHMI Drosophila EST Project
LD28056.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD28056 5prime, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA One Cyclotron Rd, Berkeley, CA 94720, USA Pax: 510 486 6098
Email: http://www.fruit/ily.org/EST, est@fruitfly.berkeley.edu Plate: 280 row: E column: 8 Plate: 280 row: E column: 8 High quality sequence stop: 400.
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69;
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/orqanism="Drosophila melanogaster"
/db_xrel="taxon:7227"
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/lab_host="DH5-alpha TonA"
/note="Organ: embryo: Vector: pFlc1; Site_1: Xho1; Site_2:
BamH1; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
185 c 187 g 99 t lothers
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                                                                                                                                                                                                                                                         /clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/sex="male and female"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachlycera;
M.scomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 626)
Hurvey, D.; Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
                                                        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003438: arm:X [6347108,6646644]
estimated-cyto:6B1-6D3: 04/11/2001
Plate: RE.43 row: D column: 7
High quality sequence stop: 490.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 466 6798
Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
plate: 379 row: E column: 10
High quality sequence stop: 413.
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XLI Blue"
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/db_xref="taxon:7227"
/clone="RE04343"
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/db_xref="taxon:7227"
/clone="LD37958"
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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69;
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Best Local Similarity 100.0
Matches 19; Conservative
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1 (bases 1 to 650)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champer,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,M., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
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                                                                                                                                                                                                                                                                                                   BI168066 650 bp mRNA EST 09-JUL-2001 RE08607.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE08607 5 similar to CG4532: FBan0004532 located on: X 6D1-6D2;: 04/11/2001, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003438: arm:X [6347108,6646644]
estimated-cyclo:681-683: 04/11/2001
Blate: RE.86 row. A column: 7
High quality sequence stop: 515.
                                                                         Gaps
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/lab_host="DH5-alpha TonA"
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                     Length 626;
                                                                         Indels
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/organism-"Drosophila melanogaster"
/db xrel "laxon:7227"
/clone-"REORGO7"
                                                                      ;
                     10;
                DB
70;
                                                                      Mismatches
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                   Score 19;
Pred. No.
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4.2%; Scc.
100.0%; Pre
0;
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Contact: Stapleton, M.
                                                                                                                       417 ccacgacggqctgctggcc 435
                                                                                                                                                563 CCACGACGGCTCCTGGCC 581
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                                                                                                                                                                                                fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 742)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
                                        AA941556 742 bp mRNA EST 23-APR-2001 LD25548.Sprime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD25748 5 similar to CG4532: FBan0004532 located on: X 6D1-6D2;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003438: arm:X [6347108,6646644]
estimated-cyto:6B1-6D3: 04/10/2001
Plate: LD.257 row: D column: 12
High quality sequence stop: 605
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/db_xref="taxon:7227"
/clone="LD25748"
/clone_lib="LD Drosophila melanogaster embryo pOF2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                     On May 1, 1998 this sequence version replaced gi:3101469.
Other_ESTs: LD25748.3prime
Contact: Stapleton, M.
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4.2%; Score 19; DB 10; Length 742;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels
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One Cyclotron Rd, Berkelny, CA 94720, USA
Fax: 510 486 6798
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/siran-"Japonica"
//db_xrei-"laxon:4530"
//clone_"hbxp0046Hil5"
//clone_"hbx0046Hil5"
//clone_"hbx1"E. coli bH10B"
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//lab.bost="c. coli bH10B"
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//hib.e="Vector: pbelouAcl2; Site_1: hindIII; Site_2: pbelouAcl2; Makel
//hib.e="Vector: pbelouAcl2; Site_1: pbelouAcl2; PbelouA
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100.0%; Pred. No. 70;
Live 0; Mismatches 0; Indels
                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwhigeclemson.edu
Seq Primer: TAATACGACTCACTATAGG
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/strain="Japonica"
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Location/Qualifiers
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                                                         Contact: Wing RA
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Search completed: April 3, 2002, 01:30:31 Job time: 9850 sec

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AC084064 Homo sapl
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Unpublished
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AE001819 Mycobarle
AE007028 Mycobarte
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AR147694 Sequence
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AC023212 Homo s
AC021263 Homo s
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynabacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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MLC91779
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AE007160
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MTCY9F9
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                                                                                             April 2, 2002, 22:44:13; Search time 2977.34 Seconds (without alignments) 2510.033 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AIDPSRLYDDELCWAPKHTDFERRALRTIDMYRDNESMLASLKHAGGRXYQDAGG"
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7002. 34 Copies in M. tuberculosis genome; Found in the rfb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3.4 sites of the genome of M. tuberculosis; present at 3.4 sites of the genome of M. H37RA, Erdman, and many isolates; not found in M. smegmatis & M. avium."
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  Direct Submission
Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
705-035, South Korea
3 (bases 1 to 3453)
                                                                                                                                                 College of
Namku, Taeg
                                                                                                                                  Direct Submission
Submitted (14-M02-1997) Tae-Yoon Lee, Microbiology, Colleg
Submitted (14-M02-1997) Tae-Yoon Lee, Microbiology, Namku,
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku,
705-035, South Korea
Sequence update by submitter
On Aug 14, 1997 this sequence version replaced gi:1304703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGGCPSLSDRDAAAPSFEEDVRRGLLPGGTDVSRFIGEMRGT"
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Length 3453;

DB 1;

Score 415.8;

91.8%;

Query Match

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3
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Mahairas, G.G., Subo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K. Molecular analysis of generic differences between Mycobacterium Dovis HCG and Virulent M. Lavis 5.
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Journal of Description 1604)

Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Mahairas,G.G., Sabo,P.J., Hickey, Molecular Microbiology, Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /note="site of deletion breakpoint in this organism. Virulent M. bovis has additional 10 kbp at this site" 637~\rm c 416~\rm g 214~\rm t
                                                                                                                                                            358
                                                                                                27-APR-1996
                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes; Actinobacteria, Actinobacteridae, Actinomycetales; Corynebacterineae, Mycobacteriaceae, Mycobacterium; Mycobacterium Luberculosis complex.
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Mycobacterium bovis BCG DNA flanking deletion region 3.
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             Indels
             5;
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Pred. No. 4.6e-56;
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0; Mismatches
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/db_xref*"taxon:1765"
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U35021.1 GI:1049243
                 450; Conservative
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Mycobacterium
                                 Microbiology,
WA 98119, USA
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Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and St Molecular analysis of genetic differences between Mycobovis BCG and virulent M. bovis G.D. 1274-1282 (1996)
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misc_difference replace(1400: .9281,")
//note="absent in related avirulent strain M.
COUNT 1706 a 3191 c 2929 g 1453 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 410; DB 1; Length 9281;
Pred. No. 2.2e-56;
0; Mismatches 5; Indels
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Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C.
Direct Submission
Submitted (29-40G-1995) Mark J. Hickey, Molecular
PathoGenesis Corp., 201 Elliott Ave. W., Seattle,
Location/Qualifiers
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U35017.1 GI:1049238
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Conservative
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Best Local Similarity 98.0
Matches 447; Conservative
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Veterson, J., DeBoy, R., Bodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberd, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Bill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            point mutation,
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280 of the
tggatgtgtccacccyccaggccqccgaayccyacctqccggcaaaggc--ctcaatat.c
                                                                           Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
Bacteriu; Firmicutes; Actinobacteria; Actinobacteridae;
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/strain~"CDC1551"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-ARR-2001) The Institute for Ge Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          AE006921 9764 bp DNA
Mycobacterium tuberculosis cDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:83331"
/note="clinical strain"
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AE006921 AE000516
AE006921.1 GI:13879142
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/ LLD AT LET . VITTA DO / 71 + W.

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/ LULY BE ALDIO - WITTA VTCEHHAS VQRIQLRISGMSCSACAHRVESTLNKLPGVRA
AVINCTRNATIUTS ENVIRAAL (CQAVRRAGYQADLCTDDGRSASDPDADHARQLLIRL
ALAAVLFVEVADL.SVMFGVVLATRETGMQWVLSALALLBYVTWAAMBPHRVAMRINARHH
ASAMETLI SVGTTAATT WISLLYTFGNISPIERSGIWQALLGSDA IY FEVAAGVTVFVL
AGANGLIANDGSANIALIAALSAKEVAVILLDGSERVI PADHELKEQURFVVRPGQI
VGRYFERAKAS GOGSANIARIA. LAALSAKEVAYULIABLATTAGGUL I VEAAAVGADIVQF
VAANGLAVIOKARAVGRANGKLANIRISSVFRPAVIVI NALTAAGGUPRAVSAAL
AGUNTUSPQAQONGANAVALAINETSSVFRPAVIVI NALTAAGGUPRAVSAAL
AGUNTUSPQAQONGANAVALAATENSSKRSHSSENSVALAI AAATTRRDAVTDFRAI PGRG
GRIJVSGAVTAARGWEALDVALAIATTREDAVTERTA PGRG
GRIJVSGAVTAARGWEALDVALAIATTREDAVTER OF TORGEGOVI AVAD
VSGTVSGRAVRVGK PSWIGSSSCHPWIRAARRHAESIGETAVVEVEDOEPCOVI AVAD
LAKRATHRITVKLNMVAFGYNI AAI PVAAAGLINPLVAGAAMAFSSFFVVSNSI KIJKKF
GRYPLGGGTVGGOWTPAPSSA
GRYPLGGGTVGOWTPAPSSA
GRYPLGGGTVGOWTPAPSTA
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TGRTDITELTLACGPDNRLAESKGWTTHKNTHGHTEWLPPPHLDHGQPRTNTFHHPERF
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TGGSAA"
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3 3103 c 3360 g 1748 t
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OPRITYGTHITGDQVLHGERTRNRLHHELGGMAVEMEGGAVAQICASFDIPWLVIRAL
SDLGGADSGQVENRFVGEVAASSARVILRLIPVLTAG"
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/codon_start-1
/rransl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence similarity; putative"
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complement(8232, 19095)
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                                                                                                                                                                                                                                                                              /qene="MT0101"
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RWRWEFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GP:145427; identified by sequence
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                                                                                                                                                                                                                                                                                                                                                                      by Glimmer2; putative"
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                                                                                                                                                     similarity; putative"
1449. .2123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                /note="identified
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/gene="MT0096"
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adenosylmethioninc-8-amino-7-oxonomanoate
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1810, .3123
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4277. .4957
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Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
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Mycobacterium bovis BCG putative
adenosylmethionine-8-amino-7-oxononanoate aminotransferase (bioA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovis BCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                               9190 TGGATGTCCACCGCCAGGCCGCGAAGCCGACCTGGCCGGCAAAGCCGCTCAATC 9131
                                                                                                                                                                                                                                                                                                                                                                 tggatgtgtccacccgccaggccgccgaagccgacctgccgccaaaggc--ctcaatatc 118
                                                                                                                                                                                                                                                                                                                                          178
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                                                           Gaps
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                                                                                                              1 gatcggcgagggcgcacatcaaagtgattcgcgccctttttcgcccacctgcccgccgcgg 60
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1 (bases 1 to 10019)

19.5. and Jacobs, W.R. Jr.

Cloning, sequencing, and identification of Mycobacterium bovibiotin biosynthetic genes by complementing two Mycobacterium
                                                                                                                                              gtoccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacggcg
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Length 9764;
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| Mo_xref="taxon:33892"
| complement(299. .1038)
| /note="ORF1; similar to MTCY336.37"
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Score 410; DB 1; I
Pred. No. 2.1e-56;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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90.5%;
98.0%;
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                          Best_Local Sim:larity 98.0
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELGQHNGLPVSIVVTTTLDLQTGAGKGFTGGGTLLPMADVIRMTSHAHHYSPASGR
YPQAIFDHGTPLALYHTKRLASPAQRIMLFANDRGCTKPGCDAPAYHSQAHHVTGWTS
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SCAMLTABOVDQLAARGVHXVNHULFTRARSPENVYTTHYNERWOYISAWRAAGME
VCCGGILGMGETLOARERAALAEIGPDEVPLNEINWIRPGTPFADILJVWPVGDALKA
VAAFRLALPRTMLRFAGGREITLGDLGAKRGILGGINAVIVGNYIJTIGKPRABDLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGRTDITDLTLACDPDNRLAEKGWTTRKNTHGHTEWLPPPHLDHGQPRTNTFHHHEKL
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RLRYGALDFDTVPLSRGDHALTYVTQAPPVFFARRPLQIALTLMWPAGIASLVYALLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8825. .9406
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                                                                                                                                                                                                                                                                      complement(5612. .6478)
/note="ORF7; similar to MTCY251.13c"
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                                         4957. .5466
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/transl_table=11
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/transl_table=11
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/translation="RWAGRDMGDFLDEPLEDILSTPEVSHVFGDTKLGSAVPTPPVLI
VQVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSLHPLSAPWTLRWLTDRFA
GRPLTDHRVTTWPTIFNPWTYAGMNATAVIAAKVITGRKLSRRPL"
3134 c 3655 g 1774 t
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Direct Submission
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Myrobacterium tuberculosis (1x1551, section 114 of 280 of the
                                                                                                                                                           Gaps
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                                                                                                                                                                                        1 gatoggcyaggcgcacatcaaagtgattcgcyccttttcgcccacctgcccgcggg
                                                                                                                                                                                                                                                                                            6573 TGGATGTCCACCCCCCCCCCCCCCCAAGCCCAACCTGGCCGGCAAAGCCGCTCAATATC
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                                                                                                                     90.5%; Score 410; DB 1; Length 10019; 98.0%; Pred. No. 2.1e-56; ive 0; Mismatches 5; Indels 4
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Mycobarterium tuberculosis Chr1551
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AE007028 AE000516
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FEATURES

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RGATVLAHNYOLPAIODVADHYGDSLALSRYAAEAPEDTIVFGGVHFWAETAKILSPH
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HPDAELEVHPEGGGATSALVLAGEGAFPAERVKILSYGGMLEAAHTRARQVLYATEV
GMLHQLRRAAPEVDFRAVNDRASCKYMKMITPAALLRCLVEGADEVHVDPGIAASGRR
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gvvpybyatpelipadytkmhpvssleppmafdhgpmythartrliakmsytnigfalapke
falstlkolygaalkytqubatnlorvlarkkvitgtgtiaosgregggrealysefds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation*"MPDGHEGSLMVEPGNLAGATGAEMIGRPPHEELQRKVRPLLPSD
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6419. 7468
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SRSISSRRAGPLRPAGHGLATPRRRPHRHRTRRQTRHHPEQPAIRRHVTAKWLPDPPPS
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TNTFHHHEKLLRHNDEDNHDQP"
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
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                                                                                                                                                                  1. .1//83
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P1D:456041; identified by sequence similarity; putative"
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885 ACGCCATGTCACGCTAAGTGGCTACCTCACCCCCCAAG-CGCGGCCCACCTTTGAAGC 827
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                                 similarity; putative"
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Sequence 1 from patent US
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                                                                                                                                 Length 1535;
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Ribey L.W. and Chong, P.
DNA molecule fragments encoding for cellular uptake of Mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 1 01-MAY-2001;
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97.8%; Pred. No. 8.3e-56;
ive 0; Mismatches 6
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1 (bases 1 to 1535)
Riley,L.W.
DNA molecule encoding for cellular tuberculosis and uses thereof
Patent: US 6008201-A 1 28-DEC-1999;
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                                                      Location/Qualitiers
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Bacteria; Firmicutes; Actinobacterineae;
Actinomycetales; Corynebacterineae; Mycobacterium; Mycobact
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Submitted (11-JUV-1998) Submitted on behalf of the Mycobacterium
submitted (11-JUV-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence Version replaced g1:2117233.
Notes:
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                                                                                                                                                                                                                                                                                                                   Deciphering the biology of Mycobacterium tuberculosis from the
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  Score 408.4; DB 6
Pred. No. 8.3e-56;
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Nature. 393 (6685), 537-544 (1998)
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ilarity 97.8%;
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/qene="Rv1565c"
/note="Rv1565c" (MTCY336.38), len: 729. Unknown membrane
/note="Rv1565c" (MTCY336.38), len: 729. Unknown membrane
protein, some similarity to 005402 HYPOTHETICAL 72.2 KI)
PROTEIN from B. subtilis (634 aa) opt: 384 E(): 4.8e-17;
PROTEIN from B. subtilis (634 aa) opt: 384 E(): 4.8e-17;
protein in H.influenzae. N-terminal half hydrophobic.
FASTA results, Ya2_LMEIN P43993 hi0392 (245 aa) opt: 265;
E(): 5.5e-10; 28.3% identity in 247 aa overlap. TBparse
                                              available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TH genes Gene prediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rvi566c, (MTCY336.37), len: 230. Function: unknown probably exported has QQAPV repeats at C-terminus, similar to hypothetical M. leprae protein, to putative invasins 1,2(007390, 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_LISMO P21171. FASTA results, Q49634 COSMID B1170 (246aa) opt: 957 E(): 0,70.0% identity in 207 aa
Details of M. tuberculosis sequencing at the Sanger Centre are
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/strain="H37Rv"
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/strain-"H37Rv"
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/product="hypothetical protein Rv1565c"
/protein_id="CAB09072.1"
/db_xref="GI:2117272"
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/gene="Rv1566c"
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/clone="Y48"
33. .32091
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/gene="Rv1565c"
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                                                                                   /db_xref="SPTREMEL:006624"
/translation="WKRSWKSGSPALGLAMMLAPMVAAPGLAAADPATRPVDYQQITD
VARAGLSQRQVPFSWAGGGISGPTRGTGGITWVGPDASGLIQYAPARAGGLKLARSS
GQMYKVGQKVLPQOARKGDLIFYGPEGTGSWALYLGKGQMLEVGDVVQVSPVRTNGWT
PYLVRVLGTQPTPVQQAPVQDAAVQQAPVQQAPVQQAPVQQAPVQQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC2.6.1.62) 006622. Contains aminotransferase (EC2.6.1.62) 006622. Contains aminotransferases class-III pyridoxal-phosphate attachment site (PS00660). FASTARCENILS, BIOA MYCLE P4548 (436 aa) opt: 2534; E(): 0; 85.1%identityin 436 aa overlap. Also similar to other M. tuberculosis proteins e-g. MTCY227.12c, (449 aa). FASTA score: E():3.5e-16; 29.5% identity in 421 aa overlap. TBparse scoreis0.874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVTMTSWPSRLFAFTDNVCPPDACPLVPFGVNYYIYPVMMGGIG
AAATANTGEVSMLKGWYMSFWPIISIAVITVTSIAGYALAGFSERYWH"
3791. 5104
/gene="bloa"
3791...5104
/gene="bloa"
/note="RV1568, (MTCY336.35c), bloa, len: 437. Function:
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TFLAMSICDPHGGMHSLWTDVLAAQVFAPQVPRDYDPAYSAAFEAGI.AQHAGELAAVV
VEPVVQGAGGWRFHDPRYLHDLRDICRRYEVLLI.FDELATGFGKRTGAI.FAADHAGVSP
VEPVXQGAGGWRFHDPRYLTGTADVAHTISAGAAGALMHGPTFMANPIACAVSVASVE
LLIGQDWRRTRITELAAGLTAALDTATDVRYCGAIGVIECDRPVDLAVATPAA
LDRGVWLRPFRNLVYAMPPYICTPARITGITSAMVEVARLVGSLP"
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/db_xref="G1:2117269"
/db_xref="SMS-PROT.006622"
/translation="MAAATGGT-PEOIIAVDGAHIMHPYSSIGKEAVSPVVAVARHGAWTLINDGQPIEVLDAMSSWWTAIHGHPALINOALTTGI.KVMNHVMFGGLTHEPAAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="R11569, (MTCY336.34c), bioF, len: 386. Function probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-II.
                                                                                                                                                                                                                                complement(3030, .3036)
/note="possible RBS, AAGGAGG, for Rv1566c"
complement(3258. .3263)
/note="ASNI site: ATTAAT; probably linking fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PS00600 Aminotransferases class-III 
pyridoxal-phosphate attachment site" 
5101. 6261
               /product="hypothetical protein Rv1566c"
/protein_id="CaB09071.1"
/db_xref="G1:2117271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"hypothetical protein Rv1567c"
/protein_id="Ab809070.1"
/db_xref="G1:3117270"
/db_xref="SPTREMBL:006623"
                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv1567c"
complement(3259. .3543)
/gene="Rv1567c"
                                                                                                                                                                                                                                                                                                                                                          complement(3259. .3543)
/transl_table=11
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/gene="bioF"
5101. 67
                                                                                                                                                                                                               VOPPPFGTARSR"
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/gene="bioA"
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/qene="biof"
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/trānslalion~"MKAATQARIDDSPLAWLDAVQRQRHEAGLRRCLRPRPAVATELD
LASNDYLGLSRHPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQQFEAELAEFVGAAA
GILFSSGYTANIGAVVGLSGPGSLIJVSDARSHASLVDACRLSRARVVYTPHKNVDAVD
                                                                                                                                                                 AALRSKDEQRAVVYTDSVF-SADGSLAPVRFLLEVCRRHGALLLVDEAHGLGVRGGRG
TYPELGLABADVVWTTDSYRALGSQGGVVLGPTPVRAHLI DAARPF FIYTGLAPAAV
GAARALRVLGAPEVWRTPTT-SKALGSQGGVVLGPTPVRAHLI DAARPF FIYTGLAPAAV
GLARALRVLGAPESAVAAAAA
CLDAGVRVGCFRPPTVPAGTSRLRLTARASLANGELELARRVLTDVLAVARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis H37Rv complete genome; segment 5/162. Z74410 AL123456 Z74410.1 GI:3261600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tagatatatecercoaccagaccacagecgaagecaaccigcoggcaaagge--ctcaatate 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
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1 (bases 1 to 38380)

10 (bases, T. Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 gigetagecaaaciggregececeggegegaceaaceegaceacaceeggieate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            galeggegaggivudacaleaaayigaliegrgeetilittegeecaeetgeeegegg
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/qcne="bioF"

/note-"PbyU599 Aminotransferases class-11

pyridoxal-phosphate attachment site"

6258. .6938

/qene="biob"

6258. .6938
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 408.4; DB 1
Pred, No. 2.3e-56;
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/db_xref="G1:2117268"
/db_xref="SWISS-PROT:006621"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis H37Rv.
/transl_table=11
/product="biof"
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97.8%;
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gene
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Direct Submitssion

Submitted (11-JUW-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue dn Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:1405752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote="Rv0084, (MTCY251.02), len: 316, hyrb, similar to HYCD_ECOLI P16430 formate hydrogenlyase subunit 4 (307 au) FASTA scores, opt: 570, z-score: 591.6, E(): 2.1e-26, 13.18 identity in 305 aa overlap) and NUOH_ECOLI P3360nand dehydrogenase i chain h (325 aa) FASTA scores, opt: 207, z-score:220.7, E(): 9.5e-06, (26.5% identity in 260 aaoverlap)
Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davias,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hernsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Safandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL. http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes Gene prediction was based on a Hidden Markov Model of TB genes of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C ACMIONS: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /traislation="msylagamoigoywvgaplvigwtroyrrarwegragliopwr
DLIKOLGKROOITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPLDPSADLEAVVG
LLFLGTVALTLAGIDFOTSFGGMGASREITIRAALVEPTILLAVFALSIPAGSANLGAL
VASTIDHPGHVVSLAGOVLAFVALVIVIVAETGRLPVDNPATHLELTWVHEAWVLEYAG
PRLALVEWAAGMRLTVLLALLANLFLPWGIAGAAPTALDVITGVVAVAAKVAILAVLLA
ATFEVRLAK,RLFRVPELLAGSFLLALLAVTAANFFTVGA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
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/strain="H37Rv"
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/transl_table=11
/product="hyco"
/protein_id="CAA98920.1"
/db_xref="G1:405754"
/db_xref="G1:405754"
                                                                                                                                                                                                                                                           complete genome sequence
Nature. 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available on the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:83332"
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/clone="Y251"
6. .956
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967. .1629
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/gene="hycP"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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/gene="hyco"
1629. 3095
/gene="hyco"
/gene="hyco"
/gene="hyco"
/gene="hyco"
/note="Rv0086, (MTCY251.04), oxidoreductase, len: 488,
/note="hyco, most similar to splP77437/HYF_ECOLI HYDROGENASE-4
COMPONEW F(EC 1.- (526 aa), FASTA SCORES: opt: 948
Z-SCORC: 1117.4 E(): 0; 35.9% identity in 493 aa overlap.
Also similarto E. coli d9087711 & NUOL_ECOLI P33607 nadh
deliydrogenasei chain 1 (613 aa) FASTA SCORES: opt: 360,
Z-SCORE: 354.9, E(): 3.2e-13, (27.9% identity in 488 aa
overlap), and to NUON_ECOLI P33608, nadh deliydrogenase chain in (425 aa), FASTASCORES: ope: 375, Z-SCORE: 371.4,
E(): 3.9e-14, (25.0% identity in 432 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hype"
//product="hype"
//protein_id="CAA98921.1"
//db_xref="ali:1d05755"
//db_xref="sulss-prot:010882"
//db_xref="su
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VYLFLAGYPDRRVELEYVVPADNPEIRSLAYLSFPAGRFEREMADLYGRPVGHPKPR
RLVRHAHWPDWHPMRTDAGPAPEFTDTGAFPFLAVEGPGVYEIPVGPVHAGLIEPGHF
/note="Rv0085, (MTCY251.03), len: 220. hycp, similar to splP77524|HYFE_ECOLI HYDROGENASE-4 COMPONENT E (216 aa), FASTA scores: opt: 204 z-score: 272.1 E():1.2e-07; 25.5% identity in 216 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Another—RAD087, (MTCY251.05), oxidoreductase, len:
Aug. hycE, similar to HYCE_ECOLI P16431 formate
hydrographyses submini 5 (569 ab PASTA scores, opt. 680,
2 score: B08.1, E(): 1.8c 38, (31.2% identity in 449 aa
overlap) and to NUOD_ECOLI P33600 nadh dehydrogenase i
chain 4, (407 aa) PASTA scores, opt: 245, z-score: 293.1,
E(): 8-9e-10, (24.5% identity in 368aa overlap)"
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/4605, English
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/gene="hyce"
3092. .4570
/qene="hyce"
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/db_xref="taxon:83332"
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1. .43401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="H37kv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Rv3448"
78. .164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Y77"
78. .1481
                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 43401)
                                                                                  43401 hp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiation codon.
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                             DEFINITION
                                                                                                                                                          ORGANISM
                                                                                                            ACCESSION
                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                   AUTHORS
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                                                                        MTY13E12
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                                                                                                                                                                                                                                                                                                              /translation="MDOPWNNIHYDALLDAWYPLGTOCVLDVGCGDGLLAARLARRI
PYVTANDIDAPVLRRACTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
PPQTLHELREHVRALLPGACIRRLLYGRVLVTWRAPV"
                                                                                             GREEYRAVKPGTPGIQPKGDMMYNYVDAGPGRVSRSYEVAAPAAELFAIVADPRRHR
ELDGSGTVRGNIKVPAKLVVGSKFSTKMKLFGLPYRITSRVTALKPNELVEWSHPLGH
RWRWBFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
                                                                                    /translation="MSVYKHAPSRVRLRQTRSTVVKGRSGSLSWRRVRTGDLGLAVWG
                                                                                                                                                                                           12406 GATCGGCGAGGCGCACGTCAAAGTGATTCGCGCCTTTTTCGCCCACCTGCCCGCGCGG 12347
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rv0090, (MTCY251.08), len: 256. Unknown."
                                                                                                                                                                                                                                                                                                                                                   6147. .6152
/note="abggag, potential rbs upstream of Rv0090"
6158. .6928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 38380;
      'note="Rv0088, (MTCY251.06), len: 224. Unknown"
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                                                                                                                                                                                                                                                               /product-"hypothetical protein Rv0089"
/protein.id="CAAA8925.1"
/db_xref="G1:1405759"
/db_xref="SWISS-PROT:010886"
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/transl_table=11
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                                        /product="hypothetical protein Rv0088"
/protein_id="CAA9824.1"
/db_xref="GI:1405758"
/db_xref="SWISS-PROT:010885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 408.4; DB 1;
97.8%; Pred. No. 2.2e-56;
tive 0; Mismatches 6;
                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv0090"
/gene="Rv0090"
6158. 60.
                                /transl_table=11
                                                                                                                                                 5436. .6029
/gene="Rv0089"
5436. .6029
/gene="Rv0089"
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/gene="Rv0090"
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                      /codon_start=1
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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes implemented in TBparse (kroyh) supplemented with visual inspection of positional base preference in endowing specially where there is an interease in the observed/expected third position of 4C an interease in the observed/expected the correct initiation codon. Where possible we choose an initiation codon (algorithms) give sequence (optimally 5-13bp before the initiation codon planding site sequence (optimally 5-13bp before the initiation codon in it this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 15A Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:2104370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry Ill, C.E.,
Harris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry Ill, C.E.,
Connor, R., Dadcock, K., Basham, D., Chillingworth, T.,
Hamlin, H., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quall, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sacs, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B.G.
                   Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.
295390 AL123456
295390.1 G1:3261766
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deciphering the biology of Mycobacterium tuberculosis from the
03-AUG-2001
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/note="PS00402 Binding-protein-dependent transport
systemsinner membrane comp signature"
                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Nature, 393 (6685), 537-544 (1998)
98295987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable precursor of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 053863 SERINEPROTEASE (1990 aa) pot: 241; E(): 8e-07; (38.0% identity in387 aa overlap), similar to MTCY15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                         /traislation="MPTSDPGLRRVTVHAGAQAVDLTLPAAVPVATL1PSIVDILGDR
GASPATARYGLSALGAPALPNATTLAQCGIRDGALVLHKSSAQPPPRCDDVAEAV
GAADDTTARPCQCATRISGALASCITAGGGLMLVRNALGTNVTRYSDATGCVAAA
GLAALLTRAVACRTYRDIAGLTLSVIATIFGAVAGLLLAVPGVPGVHSVLVAAMAAAA
TSVLAMRITGCGGITLTAVACCAVVVAAATLVGAITAAPVPAIGSLATLASFGLLEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAALAYAVDYKNAY IYAAAGNIGGAAQCPPOABGUTRBSVIVAVSPAWYDDY LLIVGS
VAQGEPSATLAGPWUDVAATGEAYSLSPFGDGTVRRLGOGHSS IL SGTSYRAPV
VSGLAAL IRARFPILTAROWMGT IESYTÄHPPAGWDEN/GNGTOGHALAAVSSDS IPOA
GTATSDPAPVAVPVPRRSTPGPSDRRALHTARAGAAICLLALMATLATASRRLRPGRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARMAVILLAGISPRLPPALNPDDADALPTTDRLTTRANRADAWITSLLAAPAASATIGA
IGTAVATHGIHRSSMGGIALAAVTGALLLLRARSADTRRSLVFAIGGITTVATAFTVA
ADRALEHGPWIAALTAMLAAVAMFLGFVAPALSLSPVTYRTIELLECLALIAMVPLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="WITSRTERLLVVSALATLSGLGTPVAHAVSPPP IDERWLPESAL
PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGAGGRVAVIDTGVA
RHRRLPRVVAGGDYVFTGDGTADCDAHGTLVAGIIAAAPDAQSDNFSGVAPDVTLISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQSSSKFAPVGDPSSTGVGDVDTMAKAVRTAADI.GASVINISSIACVPAAAAPUDKAL
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                                                     Unknown membrane
                                                                       protein, contains PS00402 Binding-protein-dependent transport systems inner membrane comp signature. Some similarity to ALO21930|MTV035_1B Mycobacterium tuberculosis (Laa) fasta score, opt: 429 z-score: 488.4 E(): 1.1e-19; 28.2%identity in 479 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="RV3449, (MTCY13E12.02), len: 455. Function:
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/gene="Rv3449"
/note="PS00136 Serine proteases, subtilase family,
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                                               467 aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein Rv3449"
/protein_id="CAB08735.1"
/db_xref="GI:2104372"
/db_xref="SPTREMBL:006316"
                                                                                                                                                                                                                                                                                /product="hypothetical protein Rv3448"
/protein_id="CAB08736.1"
                                               /note="Rv3448, (MTCY77.20),
                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:3261767"
/db_xref="SPTREMBL:033354"
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1862. .1894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:83332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLCGAYSAVRHLDLTWT"
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/transl_table=11
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1478. .2845
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/gene="Rv3449"
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/gene="Ry3449"
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VVVGPAEDSSAQVLITAEQM ILVATESGSPTYLLYGGRRAVVDLADPAVWALRLQGRV
PHVVAQSLLNAVPEAPRITAPRIRGGGRASVGLPGFLVGGVRITRASGDEYYVVLED
CVQRTGQVADALLREUSGGSNVNPPTVAPDVITRAPIVNTLAPDRPPTPVDGSP
GRAVTTLCVTWTPAQDGARAVELASGEPVPLGGVPVTLAQADGGRGFALDAVYLPPG
RSAYVARSLSGGGTGTRYLVTDTGVRFAIHDDDVAHDLGLPTAAIPAPWVLATLPS
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LSPLEGSKALDLCHPTDPLCHVGPGNEFSGHIDGYIPTYTQAASFVVQRLRAGSVPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALGCYLATVAAMGCAFVALLRPQSALGQAPIVMGRESGALYVKVDDVWHPVLNLASAR
LLAATNANPQPVSESELGHTKRGPLLGIPGAPQLLDQPLAGAESAWAICDSDNGGSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGRVGQAFVDSLRQQFGMETGVYPVNYAASRLQLHGGDGANDATSHTKSMASSCPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MPSPATTWLHVSGYRFLLRRIECALLFGDVCAATGALRARTTSL
unknown but similar to Rv3895c MTCY15F10.17 (FASTA score: 1.6e-27; 36.4% identity in 475 aa overlap); possible membrane spanning region near N-terminus, and to Y4967[MLCB628_16 Mycobacterium leprae cosmid B628; (481 aa) opt: 708 z-score: 710.9 E(): 4.5e-32; 32.9% identity in 480 aa overlap, also similar to Rv3869 (MTV027.04)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cutinase, similar to several, contains cutinase, ser ine active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU Q50664 probable cutinase cy339.008c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCY13E12.05 (FASTA score: E(): 0; (59.2% in the second start of the second se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15625 GATCGGCGAGGCGCACGTCAAAGTGATTCGCGCCCTTTTTCGCCCACCTGCCCGCCGCGG 15684
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/qene="Rv3450c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
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/product="hypothetical protein Rv3450c"
/protein_id="CAH08716.1"
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/db_xref="SPTREMH1:006317"
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/protein_id-"CARN8717.1"
/db_xref-"G1:2104<sup>374</sup>".
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/note="possible RBS, GAGG, for Rv3452"
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/transl_table=11
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/gene="Rv3452"
5178. .5858
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/qene-"Rv3451"
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/gene="Rv3451"
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Firect Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualiflers
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15685 TGGATGTGTCCACCCGCCAGGCCGCCGAAGCCGACCTGGCCGGCAAAGCCGCTCAATATC 15744
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                                                         accteaccgacacegaacgcgccgcaaacgc-gcatcaccctgagcaaccagcaatacg
                                       gtcccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacggcg
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Mycobacterium tuberculosis CDC1551
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/product="serine esterase, cutinase family'
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96. .839
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// ranslation="MMPGVITNSESPTATRETRESSPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTAGNSESPTATRETRESSPTAGNSESPTATRETRESSPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTAGNSESPTA
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/db_xref-"GI:13883394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.PGSVPQLPGSVLQMPGTAAPAPESLHGR
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/note-"identified
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3;

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PRDLTEEQLIHLRDYIEANLKVEGDLRREVQADIRRKIEIGCYQGLRHRRGMPVRGQR
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                                                                                                                                                                                                                                                                                                                                                                                         11392 TGGATGTGCGACCCGCCAGGCCGCCGAACCGACCTGGCCGGCAAAGCCGGTCAATATC 11451
                                                                                                                                                                                                                                                                                                                                                      tquatqlqtccarreqeeqqeeqqeeqqaqregacctgccggcaaagge--ctraatatc 118
                                                                     complement(7719. .7832)

Agene-MT3567.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acggcatgtcacggctaagtggctacctgacccccaagtcgcgggccacctttgaagcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accteaecgaeacgeaegeaegeaege-geateaeectgageaaeeageaataeg
                                                                                                                                                                                                         Length 16384;
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                                                                                                                                                                                                   Score 403.6; DB 1;
Pred. No. 1.8e-55;
D; Mismatches 9;
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Pred. No. 1.3e-49;
0; Mismatches 12
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Stover, C. Kendall and Mahairas, G.G.
                              complement(7719. .7832)
/gene="MT3567.1"
                   TKTNARTRKGPKRTIAGKKKAR"
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1. .12412
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/transl_table=11
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186264
                                                                                                                                                                                                     89.18;
llarity 97.18;
Conservative
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95.6%;
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Best Local Similarity 95.6
Matches 432; Conservative
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                                                                                                                                                                                                                                          Matches 443;
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Best Local S
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ORIGIN
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TITLE
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KEYWORDS
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/ gene="Milar to SP:P81288; identified by sequence similar to SP:P81288; identified by sequence similarity; putative"

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FRUDDSIYSPVLKVTXVDARTRUGRFREDFMILLILDVEFKNSISPRDALASAGKTLEVEL
FGLARELNVERGEIGFSPRAADHTASFALPIDDLDLITVRSYNCIKREGYHTVGELV
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                                                                                                                                                                                                                                                                                                                /gene="MT3564"
/note="similar to SP:P72404; identified
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase,
                                                                                                                           L17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ribosomal protein S11"
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                                                                                                                                                                                                                                                         complement(4897. .5940)
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complement(4897. .5940)
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complement(6092. .6697)
           complement(4323. .4865)
/gene="MT3563"
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complement(6706. .7125)
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/product="DNA-directed
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 aggegeacateaaagtgattegegeeetttttegeee--acetgeeegeegegggatg
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tuberculosis and uses thereof
Patent: US 6008201-A 5 28-DEC-1999;
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258 c 185 a
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al Similarity 97.7%;
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llarity 97.7%; Pred. No. 1.4e-46;
Conservative 0; Mismatches 5;
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Sequence 5 from patent US 6224881.
AR147696 GI:15111786
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258 c 185 α
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Riley, L.W. and Chong, P.
DNA molecule fragments
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Job time: 12522 sec

4.5 Compugen

GenCore version Copyright (c) 1993 - 2000

- nucleic search, using sw model

OM nucleic

on:

hits satisfying chosen parameters: 1472140 seqs, 8248589755 residues

Total number of

Searched:

IDENTITY\_NUC Gapon 10.0 , Gapext 1.0

Perfect score:

Sequence:

Scoring table:

Maximum Match 100% Listing first 45 summaries

gb\_ba:\*
gb\_htg:\*
gb\_in:\*gb\_om:\*
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Database

90\_ph: \*
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90\_vi: \*

em\_fun:\* em\_hum:\*

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em\_pat: \*
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em\_pl: \*
em\_pl: \*

em\_sts:\*

em\_sy:\*

Post-processing: Minimum Match 0% Maximum Match 100%

sed length: 0 seg length: 2000000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_htg\_other:\*

em\_htg\_inv:\* em\_htg\_rod:\*

em\_un:\*
em\_vi:\*
em\_htgo\_hum:\*
em\_htgo\_inv:\*
em\_htgo\_rod:\*

SUMMARIES

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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
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/product="hypothetical protein Rv3448"
/protein id="CAB08736.1"
/db.xref="g1:326176"
/db.xref="sPTRBME:033354"
/translation="MPTSDPGLRRVTVHAGAQAVDLTLPAAVPVATLIPSIVDILGDR
GASPAPAARYTRLSGALGAPANATTHAGALASCITAGGGLMLVRNALGTRWTKSGAPATARCDVVAAA
GLAALLFAVIACRTYRDPIAGLTLSVIATIFGAVAGLLAVPGVPEVHSVLVAAMAAAA
GLAALLFAVIACRTYRDPIAGLTLSVIATIFGAVAGLLAVPGVPEVHSVLVAAMAAAA
                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JUW-1918) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
on Jun 27, 1998 this sequence version replaced gi:2104370.
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ARMAVLLAGLSPRLPPALNPDDADALPTTDRLTTRANRADAWITSLLAAFAASKTIGA
IGTAVATHGIHRSSMGGIALAAVTGALLLLRARSADTRRSLVFAICGITTVATAFTVA
ADRALEHGWNIAALTAAMLAAVAMFLGFVAAPALSLSPVTYRTIELLECLALIAMVPLTA
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Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
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                                                                Deciphering the biology of Mycobacterium tuberculosis from the
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/gene="Rv3448"
/note="ps00402 Binding-protein-dependent transport
systemsinner membrane comp signature"
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/organism="Mycobacterium tuberculosis H37Rv"
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/strain="H37Rv"
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Nature. 393 (6685), 537-544 (1998)
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/clone="Y77"
78. .1481
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                                                                                                                                                                                                                                                                                                                 probable precured of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PSO0136), histidine active site (PSO0137), serine active site (PSO0138). FASTA results: 963863 sERINEPROTEASE (390 aa) opt.: 241; E(): He-07; (38.0% identity in387 aa overlap), similar to MTCY15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSSSKEAPVGDPSSTGVGDVDTMARAVRTAADLGASVINISSIACVPAAAAPDDRAL
GAALAYAVDVKNAVIVAAGNTGGAAQCPPQAFGVTRDSVTVAVSPAWYDDVYLTVGS
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CTATSDPAPVAVPVRRSTPGPSDRRALHTAFAGAAICLLALMATLATASRRLRPGRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lrans lation="MTMTSRTLRELTVVSALATLSGLGTPVAHAVSPPPIDERWLPESAL PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGAGQRVAVIDTGVA RHRRLPRVVAGGDYVFTGDGTADCDAHGTLVAGIIAAAPDAQSDNFSGVAPDVTLISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4049. .4081)
/gene="Rv3450c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site"
                                                                                                                                                                                                                                                                                   (MTCY13E12.02), len: 455. Function:
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1862. .1894
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/gene="Rv3450c"
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/transl_table=11
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Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds. U43540 U43540. GI:2326948
                                                                   geceaacycaaccacagetgetgecqqeeqqetgecqcqcqcqctgatcgeetccqygaaa
accoggiteatequaccaceceegalgegaegecategaeegegaeaceegeagecaa
                                   caccccgacggcgacctcaccgaccgcaacgcgcccgcaaacgcggcatcacctgagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16632 AAACCCGATTGAC 16644
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KEYWORDS
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GIGRYGQAFVDSLRQOTGMELGVYPVNYAASRLQLHGGDGANDAISHIKSMASSCPNT
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LSPLFGSRAIDLCNPTDPICHVGPGNEFSGHIDGYIPFYTTQAASFVVQRLRAGSVPH
                                                                                                                                                                                                                                                                                                                                                 0
                                                                probable cutinase, similar to several, contains cutinase, serine active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU Q50664 probable cutinase cy399.08c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCY13E12.05 (FASTA score: E(): 0; (59.2% identity in 211 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv3452, (MTCX13E12.05), len: 226. Function:
probable cutinase precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                       /note="PS00155 Cutinase, serine active site, 5165. .5168
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; Pred. No. 5.4e-181;
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BS, GGAG,
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4388 .5131
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4388 .5131
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100.0%;
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Matches 1393;
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AIDPSRLYDELCWAPKHTDFERALRTIDWYRDNESWLASLKHAGGRYQDAGQ"
                                                                                                                                                                                                                                                                                         of
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2202. 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee,T.
Direct Submission
Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
7 (5-035, South Korea
3 (bases 1 to 3453)
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Namku, Taegu
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                                                                                                                                                                                                                                                                                         a novel repeated
                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaee; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology,
Daemyungdong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission

Direct Submission

Submitted (14-Aug-1997) Tae-Yoon Lee, Microbiology, Submitted (14-Aug-1997) Tae-Yoon Lee, Microbiology, Medicine, Yeungnam University, 317-1, Daemyungdong, 705-035, South Korea
Sequence update by submitter
On Aug 14, 1997 this sequence version replaced gi::

1. 3453

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150...1139
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                                                                                                                                                                                                                                                                                Rhamnose biosynthetic genes related to Mycobacterium tuberculosis
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Mycobacterium tuberculosis.
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2 (bases 1 to 3453)
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       3; Gaps
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97.28;
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    Similarity
    Best Local
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/note="3-4 copies in M. tuberculosis genome: Found in the rfb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv, H37Rv, H37Rv, and many isolates; not found in M. smeqmatis & M. avium:

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/rpt\_type=dispersed /rpt\_unit=1806, .229 | 1226 c 990 g

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QAHHVTPAWTSYGKTDITDLTLACDPDNRLAERGWTTHKNTHGHTEWLPPPHLDHGQPR
'INTFHHHERLLRHNDEDNHIDDP"
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VIQILIADBELEELI ALADEVRARWCHEVEVEGI I SLKTGGCPEDCHECSGSGLFASPV
KSAMLD ITSALVARAGOTASOATEET I VAAVWGDERIAMOVAAGI EBLIRNEVEINIA
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Mycobacterium tuberculosis CDC1551

Bacteria: Firmicutes, Actinobacteriaces,
Actinomycetales; Corpnebacterineae; Mycobacteriacese;
Mycobacterium; Mycobacterium tuberculosis complex.

I (bases I to 1783)

Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Salzberg, S.L., Delber, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Gill, J., Mikula, A. and Bishai, W.

Mycobacterium tuberculosis clinical and
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., Dedson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                             2787
                                                                                                                                   1021 atcttcgaccacggcacacccctggcgctgtatcacaccaaacgcctagcctccccggcc 1080
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AE007028.1 GI:13881250
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complement(3953. .4054)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGATVLAHNYQLPA IQDVAHHYGDSLALSRYAARAFDOOTONGLIKAALL
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SVQRMIEIGHPGGGE"
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6419. .7468
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7468. .9051
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/ rainstallon-"Magnawronauvvy igtgvaglaaalaadragksvvvi.skaaqt

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vypgahysch i opthyrmi. Stanger i skrateliagank kastolinvykgp i p

vypgahysch skratssynyred i stanger i skrateliagank kastolinvykgp i p

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i skrateliaganki. Tuvagosytaaalartesrgosyticytype
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Matches 1344;
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                                  Direct Submission
Submitted (07-JaN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"putative
adenosylmethionine-8-amino-7-oxononanoate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="2.3.1.47"
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2 (bases 1 to 10019)
Yu,S.
                                                                                                                source
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                                                         JOURNAL
       REFERENCE
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                                                                                             FEATURES
                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning, sequencing, and identification of Mycobacterium bovis BCG
biotin biosynthetic genes by complementing two Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accaacacttecaccaccegaacgattectecacaaccaagacgacgacgacaaaece 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium, Mycobacterium tuberculosis complex.

I (bases 1 to 10019)

Yu, S. and Jacobs, W. R. Jr.
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Unpublished
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SOURCE
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0; Mismatches 42;
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Best Local Similarity 97.0%;
Matches 1341; Conservative
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Mycobacterium tuberculosis CDC1551

Mycobacterium tuberculosis CDC1551

Bacteria; Firmicutes; Actinobacteria; Actinobacteriade;
Actinomycetales; Corynebacterineae; Mycobacterium: Lason, M.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dason, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Haboratory strains
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                                                                                                             906
                                                                                                                                                                                                                                                                                                                                                                                                                       cacagccaagcccaccactcaccgcctggaccagcaccggacgcaccgacatcaccgag 1206
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                                                                                                                                                                     787 cgcaaccacgacgggctgctggccgggctgcgcgctgatcgcctccgggaaactgggc
                                                                                                                          6160 CAACACAACGGTCTTCCCGTCTCGATCGTGTCACCACCACCACCACCACCACCTGACAAACC
                                                                                                                                                                                                                                                  6220 CGCAACCACGACGGCTGCTGGCTGCCGGGCTGCGCTGATCGCCTCCGGGGAACTGGGC
                                                                                                          967 atgaccagccacgccaccactactccccgcaagcgggaggtacccccaggcgatcttc
                                                                                                                                                                                                                                                                                                                                                                                      5920 ATCATGCTGTTCGCCAACGACCGCGGCTGCACCAAACCCGGCTGTGACGCACCGGCCTAC
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AE007160.1 GI:13883389
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                                                                                                                                    Genomic Research, 9712
Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
1. 16894
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//occe="similar to SP:P07649 GB:X02743 PID:41718 GB:U00096 PID:1788657; identified by sequence similarity; putative" //codon_start=1 //transl_cable=11 //transl_cable=11 //transl_cable=11 //product="tRNA pseudouridine synthase A" //protein_id="AaK47901.1" //protein_id="AaK47901.1" //protein_id="AaK47901.1" //db_xref="GI:13883394" //translation="MSLTRRPPKSPORPPRISGVVRLRLDIAVDGTDFAGWAAQVGQ RTVAGDLDAALTTIFRTPRPRSPROPAGFDARFSALRRHYVYRLSTAPYGVEPQQA RTVAGDLDAALTTIFRTPRPRSPROPAGFDARFSALRRHYVYRLSTAPYGVEPQQA RTVADAFCWSWNRSLVGALAYGEHRRATTWGRELLTATGRSSDFAVAPAHGITLIQV DYPPDDQLASRNLYTRDVRSG" complement (4323. .4865) //dene="MT3563" complement (4323. .4865) //dene="MT3563" //d
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Complement(7129. 7503)

Agene="Mr3567"

Note="similar to GP:21043%; identified by sequence similarity; putative"

Codon_start=1

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TFTAIRSLOAGLEVGAISIVYTPQPHNGVRPPKRRRV"  
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Mycobacteriaceae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

(bases 1 to 1604)
Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K.
Molecular analysis of genetic differences between Mycobacterium
bovis BCG and virulent M. Dovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
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                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                     /note-"site of deletion breakpoint in this organism. Virulent M. bovis has additional 10 kbp at this site" 637~\rm c -416~\rm g -214~\rm t
                                                                                                                                                                                                                                       1.26
                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                          186
          Stover, C.
                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caatacgacggcatgtcacggctaagtggctacctgacccccaagcgcgggccaccttt
                                                                                                                                                                                                                                        tggacgaggtqtcttttgaggtyttgaccaccagaacggctgcggtctctggaacqtc
                                                                                                                                                                                                                                                                                                                          agggeet gat eggegaggegeaegt eaaagtgatt egegeeet tit tiegeeeaeet geee
                                                                                                                                                                                                                                                                                                                  cccaagccagryayyaagaartggycggcargctgtyctgcgcggctggccaaccggttac
                                                                                                                                                            Length 1604;
                                                                                                                                                                               0;
          and
                            Hickey, Molecular
Ave. W., Seattle,
                                                                                                                                                                                Indels
          Singh, D.C.
                                                                                                                                                            1314.2; DB 1;
No. 1.2e-169;
                                                                                                                                                                                43;
                                                                  bovis
           Hickey, M.J.,
                                                                                                                                                              Score 1314.2;
Pred. No. 1.2e
0; Mismatches
                                                             /organism-"Mycobacterium
/sub_species-"HCG"
/db_xref="taxon:1765"
1400
2 (bases 1 to 1604)
Mahairas, G.G., Sabo, P.J., Hickey, M
Direct Submission
Submitted (29-AUG-1995) Mark J. Hi
PathoGenesis Corp., 201 Elliott Av
Location/qualifiers
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; 0

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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TD genes implemented in TDparse (krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (aug. gtg. or Ltg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv1565c, (MTCY336.38), len: 729. Unknown membrane protein, some similarity to 005402 HYPOTHETICAL 72.2 KD PROTEIN, from B. subfilis (634 aa) opt: 384 E(): 4.8e-17; 29.1% identity in 478 aa overlap and to hypothetical protein in H.influenzae. N.terminal half hydrophobic. From Arshar results, Y 512. HABIN P43993 hi0392 (245 aa) opt: 265; E(): 5-5-10; 28.3% identity in 247 aa overlap. Tubparse
Parkhill, J.

Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Doctcur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2117233.
Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism~"Myrobacterium tuberculosis H37Rv"
/strain="H37kv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mycobacterium tuberculosis H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mycobacterium tuberculosis H37Rv"/strain-"H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv1565c"
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/notex"re-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start-1
/transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="H37kv
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                                                                                                                                                                                                                                                                                                                                                                                                                        initiation codon.
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   AUTHORS
TITLE
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                                                                                                                                 COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctgaccctggcctgcggcccgacaaccgactcgccgaaaaaggctggaccaccacaaa 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1284 CTCACCCTGGCCTGCGACCCCGACAACGACTGGAAAAAGGCTGGACCACCGCAAA 1343
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                                                                                                                                                                                                                                                                                                                                                                                       atgaccagccacgccaccactactccccgcaagcggaggtaccccaggcgatcttc 1026
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                                                                                                                                                                                                                                                                                                                                                       1163
                                                                                                                 gaccacggcacacccctggcgctgtatcacaccaaacgcctagcctccccggcccagcgg
                                                                                                                                                                                                                                                                                                                                     cgcaaccacgacgggctgctggccgggctgcgcgcgctgatcgcctccgggaaactgggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence
Nature. 393 (6685), 537-544 (1998)
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Z95586.1 GI:3261785
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MTCY336/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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                 probably exported has QOAPV repeats at C-terminus, similar to hypothetical M. leprae protein, to putative invasins 1.1,2(007390, 007331) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_LISMO P21171. FASTA results, Q49634 COSMID B1170 (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlap. TBparse scoreis 0.890"
                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse
score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="possible RBS, AAGGAGG, for Rv1566c"
complement(3258. .3263)
/note="ASNI site: ATTAAT; probably linking fragments
B3/G6"
/note-"Rv1566c, (MTCY336.37), len: 230. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00600 Aminotransferases class-III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .3036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3259. .3543)
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3030.
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3791. .5104
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5101. .6261
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/gene="bioA"
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CDS

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/ LTAIGS LATION="MRAATQREIDDSPLAMLDAVQRORHEAGLRRCLRPRPAVATELD
LASNDYLGLSRHPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQOFE&RLAEFVGAAA
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AALRSRDEQRAVVYTDSYSADGSLAPVRELLEVCRRHGALLLVDEARIGGVRGGGRG
ILLYELGIAGAPDVVAUTTLSRALGSGGGVVLGPTPVRAHLIDAARPFIFDTGLABAAV
GAARAALRVLQAEPWRPQAVLNHAGELARMCGVAAVDDSAMYSVILGFPESAYAAAAA
CILJAGVRGFRPPTVPAGTSRLTRTAARASLNAGELELARRVLTDVLAARR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                               006621. Contains aminotransferases class in pyridoxal phosphate attachment site (PS00599). FASTA results, BIOF_WYCLE P45487(385 aa) opt: 1971; E(): 0; 80.18 identity in 381 aa overlap. Also similar to MTCV10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in
/note="Rv1569, (MTCY336.34c), bioF, len: 386. Function:
probable 8-amino-7-oxononangate synthase (EC 2.3.1.47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18109
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                                                                                                                                                                                                                                                                                                                                                                                                          /note-"PS00599 Aminotransferases class-II
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6258. .6938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1307.4; DB 1
Pred. No. 2.5e-169;
                                                                                                                                                                                             /protein_id="CAB09068.1"
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                                                                                                                                                             /transl_table=11
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6258. .6938
                                                                                                                                                                                                                                                                                                                                                                       5806. .5835
/gene-"biof"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.9
Best Local Similarity 98.4
Matches 1320; Conservative
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Arithin...

Direct Submission

**Luberculosis sequencing and mapping teams, Sanger Centre, Wellcome Luberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique 75724 Paris Cedex 15, France E-mail: parkhill@sanger ac.uk

**Moleculaire Bacterlenne, Institut Pasteur, 28 rue du Docteur Roux, On Jun 27, 1998 this sequence version replaced gi:1405752.

**Notes:**

**Details of M. Luberculosis sequencing at the Sanger Centre are available on the World Wide Web.

**Details of M. Luberculosis sequencing at the Sanger Centre are available on the World Wide Web.

**CHRL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

**Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base predictence in codons, sepecially where there is an increase in the observed/expected third position G + C.

**ANTION:** In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg., gtg., or ttg) which is preceded by an upstream ribosome codon). If this cannot be identified we choose the most upstream initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start_!
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/product="hypothesis" |
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VASTIDHPGHVVSLAGVLAFVALVIVVAETGRLPVDNPATHLELTWHHEAMVLEYAG
PRIALVEWARAGMRLTVLLALLANLELDWGIAGAAPTALDVITGVVAVAAKVAILAVLI
ATTECVFLAKLREKPVPELLAGSFLLALLAVTAANFFTVGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juster "Kythold4, (MTCY251.02), Ien: 316, hycb, similar to HYTD_ECOLI Pl64 to formate hydrogenlyase subunit 4 (307 aa) FASTA SCOLES, upt: 570, z score: 591.6, E(): 2.1e-26, (16.8% identity in 405 aa overlap) and NUOILECOLI.
FYGORAGH dehydrogenase i chain h (325 aa) FASTA scores, opt: 207, z-score:220.7, E(): 9.5e-06, (26.5% identity in 260 aaoverlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                967...1629

/gene-nhycp*

/note-"RNOOBS, (MTCY251.03), len: 220. hycp, similar to

splP77524|HYFE_ECOLI HYDROGENASE-4 COMPONENT E (216

aa), FASTA scores: opt: 204 z-score: 272.1 E():1.2e-07;

25.5% identity in 216 aa overlap"
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                            Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mycobacterium tuberculosis H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis H37Rv"
                                                                                   complete genome sequence
Nature. 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mycobacterium
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                                                                                                                                                     (bases 1 to 38380)
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967, 1629
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                    Squares, S., 8
Barrell, B.G.
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Parkhill,
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                                                                                                                                                                                                          ctgaccctggcctgcggccccgacaaccgactcgccgaaaaaggctggaccaccacaaa 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aacacccacggccacaccgaatggctaccaccacccacctcgaccarggccaacccgc 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis H37Rv complete genome; segment 5/162. 274410 AL123456 274410.1 GI:3261600
                                                                                                                                                                                            786
         caatacgacggcatgtcacggctaagtggctacctgacccccaagcgcgggccaccttt
                                                                                                                                                                                     gtcatcyacaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaa
                                                                                                                                                                                                                                                                         cgcaaccacgacggctgctggccgggctgcgcgctgatcgcctccgggaaactgggc
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MTCY251/c
LOCUS
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AUTHORS
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/yguel- nycwood6, (WTCY251.04), oxidoreductase, len: 488, note="nycwood6, (WTCY251.04), oxidoreductase, len: 488, hyco, most similar to splP77437|HYFF_ECOLI HYDROGENASE-4 COMPONENT FEE 1. (526 aa), FASTNA scores: opt: 948 z-score: 1117.4 E(): 0; 35.9% identity in 493 aa overlap. Also similarto E. coli d9087711 & NUOL_ECOLI P33607 nadh dahydrogenasei chain 1 (613 aa) FASTA scores, opt: 360, z-score: 354.9, E(): 3.2-13, (27.9% identity in 488 aa overlap), and to NUON_ECOLI P33608, nadh dehydrogenase ichain n (425 aa), FASTAScores, opt: 375, z-score: 371.4, (25.0% identity in 432 aa overlap)" //ronsl_table=11 //ransl_table=11 //product="hyco" //db_xref="flyco" //db_xref="f
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MLDNGIAATAFLLTAGVPLIVELGASLDVLFRVIVIGVLTGRRRRFFGDADLDKLRE
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SARLYGVLTPAFLCAMVLAVCANNIGVIWVAIEATTVITAFLVGHRRTRTALEATWKY
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RFSVAGETIVRLKARLWFVHRGIEKLFHGRPATAAVDLAERISGDTSAAHALA:ISLAI
EDALGIELPHEVHRLRALIVELERLYNHAADLGALANDVGYSLANAHAQRI KENLLRR
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VHPDDASAALGGCIGYVARASGLRSDARVEHPTIVLPTITGAPDGDVLARYTVRRDEF
AASAALAGHIVESHIFGEIEVAATLHPVGAESSGIGIVEGWRGTIVHRVEIDVDGRITR
AKVVDPSWFWWPALPVAMADTIVPDFPLANKSFNQSYAGNDL*
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7900... 4570

7900e... 4670

7001e... Ry0087, (MTCY251.05), oxidoreductase, len:

492.hycE. similar to HYCE_ECOLI P16431 formate

hydrogenlyase subunit 5 (569 aa) FASTA scores, opt: 680,

2-score: 808.1, E(): 1.8e-38, (31.2% identity in 449 aa

overlap) and to NUOD_ECOLI P33600 andh dehydroquenase i

Chain 6, (407 aa) FASTA scores opt: 245, z-score: 293.1,

E(): 8.9e-10, (24.5% identity in 368aa overlap)."
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Unknown"
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4605. .5279
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1629. .3095
/gene="hyco"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                         /note--Rv0089, (MTCY251.07), len: 197. unknown, some similarity to spiP12999|BIOC_ECOLI BIOTIN SYNTHESIS PROTEIN BIOC. (251 aa). FASTA scores: opt: 202 z-score: 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6147. .6152
/note="aaagaa, potential rbs upstream of Rv0090"
6158. .6928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note*"Rv0090, (MTCY251.08), len: 256. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1301.4; DB 1; Length 38380; Pred. No. 1.5e-168; 0; Mismatches 46; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPQTLHELRSHVRALLPGACIRRLLYGRVLVTWRAPV"
                                                                                                                                                       5436, .6029
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5436, .6029
/gene="Rv0089"
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/gene="Rv0090"
6158. Frr
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/gene="Rv0090"
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Conservative
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Matches 1340;
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546 KEYWORDS SOURCE ORGANISM	606 REFERENCE 12174 AUTHORS	666 12114	TITLE 726 JOURNAL 12054 REFERENCE	AUTHORS AUTHORS 11994	906 FEATURES SOURCE 11874	ttc 1026      TTC 11754	cgg 1086 gene     gene 	tac 1146 	144 1206 111 3AG 11574	adc 1266      AAC 11514	9c 1326 gene 	cc 1386 CC 11394	-2001 gene the CDS	
			3 7										AE006921 9764 bp DNA BCT BCT Wycobacterium tuberculosis CDC1551, section 7 of	ACCESSION AE006921 AE000516 VERSION AE006921.1 GI:13879142

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bbacterium tuberculosis CDC1551.

bbacterium tuberculosis CDC1551

eria; Firmicutes: Actinobacteria; Actinobacteridae;

nomycetales; Corynebacterineae; Mycobacteriaceae;

bbacterium; Mycobacterium tuberculosis complex.

bases I to 9764)

stron, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,

rson, J., DeBoy, R., Utterback, T., Weidman, J., Rhouri, H.,

J., Mikula, A. and Bishal, W.

egenome comparison of Mycobacterium tuberculosis clinical and
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PPQTLHELRSHVRALLPGACIRRLLYGRVLVTWRABV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /yene-"MT0095"
/note-"This region contains an authentic point mutation, causing a premature stop, and is not the result of a sequencing artifact; similar to SP:P16431 GB:X17506 PID:41684 PID:882614 GB:U00096; identified by sequence
                                                                                                                                                                                                                                                                                                                                                              es I.t.o 9764)
mann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., n.J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., 'J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., '9.S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Mikula, A. and Bishai, W.
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Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mycobacterium tuberculosis CDC1551"
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122. .1414
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1449. .2123
/yene="MT0096"
1449. .2123
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/codon_start-1
/transl_table-11
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/uene-"MT0098"
2280. .2873
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/qene-"MT0098"
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3002. .3772
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TGRTDITELTLACGPDNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQPRTNTFHHPERF
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                                                                                                                                                                                                                                                                             /note="identified by Glimmer2; putative"
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; Mismatches 48;
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96.5%; Pred. No. 7.7e-
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                                                                                                                                                                                      (3606)
                                                                                                                                                                                                                              complement(8232. .9095)
/gene="MT0103"
                                                                                                                                                                                        complement(8232.
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0
                                                                                                                                                                                                           /gene-"MT0103"
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Best Local Similarity 96.5
Matches 1338; Conservative
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and Stover, C.K. Mycobacterium

Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex. (bacaterium: Mycobacterium tuberculosis complex. Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Molecular analysis of genetic differences between Mycobovis BGG and virulent M. bovis 1274-1282 (1996)

JOURNAL

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REFERENCE
AUTHORS
TITLE
                     MEDLINE
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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мыркззі 9281 bp DNA Mycobacterium bovis deletion U35017

DEFINITION ACCESSION VERSION KEYWORDS SEGMENT

GI:1049238

035017.1

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SOURCE ORGANISM

ò; BCG" Microbiology, WA 98119, USA Stover, C. 126 186 246 203 263 323 306 366 383 443 426 503 486 563 546 623 909 683 999 743 Gaps 99 726 bovis cgggtagccgcgaacggattytcgaggtctttgatgcc\_trgatgccgaccgct tggacgaggtgtctttgaggtgttgaccacccagaacggctgcggtctctggaacgtc daqqarticirqiqiqaarqqriaqrixcaraqttgarqqriqacgccacgcccaacqcc gacggcgacctcaccgacaccgaacgcgcccgcaaacgcggcatcaccctgagcaaccag caatacgacggcatgtcacggctaagtggctacctgacccccaagcgcgggccacctt ; and Σ. strain Length Molecular , Seattle, Singh, D.C. Indels avirulent 3 t 2 ;; Score 1281.8; DB 1; Pred. No. 1.3e-165; 0; Mismatches 37; Query Match 92.0%; Best Local Similarity 97.2%; Matches 1304; Conservative misc\_difference source BASE COUNT ORIGIN TITLE JOURNAL 29 144 204 264 AUTHORS 127 247 187 324 307 384 367 144 427 504 FEATURES g Op á ò ò QQ ò Db Q QQ ò g Ω g δ q

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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Actinomycetales; Corynebacterineae; Mycobacterium;
Mycobacterium; Mycobacterium tuberculosis complex.

I (bases 1 to-34331)
Schoots; T., Barsch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Texia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
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Moule, S., Murphy, L., Oliver, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
Complete genome sequence
Complete genome sequence
Complete genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv complete genome; segment 50/162. 295584 AL123456 295584.1 GI:3261774
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/db\_xref="SPTREMBL:006536" /translation="MVITINRPEARNAVNGAVSIVVGDALEEAHDNPDVRAVVITGAG DKSLCAGADLKAIARRENPYHPHHGEWGIAGYRHHFIDKPTSAAVSGTALDDGAEPAL /protein\_id="CAB09023.1" /db\_xref="G1:2117173" /db\_xref="SPTREMBL:006535" /translation="MSFLVLPPEVNSALMFAGAGSGPTLAAAAAWDGLAAFLGQAANS GLANLODGINGSGUNGSFINEGTANAUSFINVGSANHGSFINVGFANLGUNNLI, LANLGNN NLAJ LANLGNINLGTGLIGGUNMIGTGALINSGTGNLGFGUNSGUNNLIGTFINSGNNNTGFFIN SCHSINFGFFINSGPLINTGFGNAGFTINTGFGNAGSGNFGFGNAGNNNFGFGNSGFENMGV GNSGAYNTGSFINSGTLINTGDLINSGDFINTGMARSGDLINTGGFFISGDLINTGFGSEVVDQPV /transl\_table-11
/product-"hypothetical protein Rv1134"
/protein\_id-"CAR09022.1"
/bc.brief-"GI:2117122"
/db\_xref-"SPTREMBL:006534"
/translation-"MAAYQKFGQEHAAAIRGGAVLHPTATATTVRVTGARGGDVVTGD FSSATAALADTAWGGPAATAMAAAAAPYASNILSTAATRALSAAAQAKAAAAVYEAARA YVDPILLYAANHIQLYSIJVISNILFGQNAPAIAAFAAFAZAYGUMADVAANYSHISOSASA VAAQLAPWAQAVKAI, PHPTARASGPAALA IPPALGIGNIG IGNIESI GNIEDVNULGN GNIGNANILGSGAYGGANI KISGNIGFFNEGSGNIANTHFGSGNI GNI ANLGSGNIGGNI MNSGFCN1GTCNSGFNNSGDANSGFQNTNTGAFFIGHSGLLNSGGCQHVG I SNSGTGF NTGLFNTGFNNTG1GNSATNAAFTTTSGVANSGDNSSGGFNAGNDQSGFFING" AlaAsn, -rich family (PPE class). Similar to etc,
MTCY98.0034c,MTCY03C7.23, MTCY13E10.17c, MTCY06H11.05,
MTCY31.06c. FASTAGOORS: MTCY9824 NID: 91781238 MYCODAGCTERIUM LUDERCULOSIS (615 aa) opt: 2292: E(): 0;
59.6% identity in 627 aa overlap. TBparse score is 0.881" 7805. 3146 79ene="Rv1136" 79ene="Rv1136" 70ene="Rv1136" 70 /note="Rv1135c, (MTCI65.02c), len: 618. Member of Gly, /note="Rv1134, (MTC165.01), len: 78. TBparse score is /organism-"Mycobacterium tuberculosis H37Rv" /organism~"Mycobacterium tuberculosis H37Rv" /note="possible RBS, AAGG, for Rv1135c" /transl\_table=11 /product="hypothetical protein Rv1136" /protein\_id="CAB09024.1" /db\_xref="C1:2117174" GPYEAADLDEQGPFPMETVYLWEDGPNGTTRMTL"

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DB 1;
                                                                                                                               699.6; DB
No. 7e-87;
                                                                                                                                                                                               0; Mismatches
                                                               /db_xref-"SPTREMBL:006540"
/protein_id="CAB09028.1"
/db_xref="GI:2117178"
                                                                                                                                   Score
Pred.
                                                                                                                                   50.2%;
                                                                                                                                                              70.48;
                                                                                                                                                                                               Conservative
                                                                                                                                                              Similarity
                                                                                                                                                                                     975;
                                                                                                                                                          Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTSYDTOLLVVOGGPGGLATALHARARGLSVIVAEPRENPIDKA CGEGLMPGGLAELTSLGVDPVGLPFHG1AYVCEHRRVQARFRTGPGRGVRTTTHAAL AARAKEQDTEWIRSRVAT1QQDAHGVTAAGVRAKWLVAADGLHSAVRRANGIKATAGT
                                                                                                                                                                                                                                                                                                                                                                           /translation="MLSARCHIRHIGSPGKDARCAHLSATLRPGIGISPTNVGNATVL
ADGTPAKPIQGAETWQRARHTGSCFSANARGPAISSGNPSRAGCGVPSSTTTPSSTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRYGVRWHYRLPVWSDFVEVHWSRWGEAYVTPVEPDLVGVATLSRORPELAWFPSLA
HHLQDASRGHARGCGPLRQVVSRRVAGRVLLVGDAAGYEDALTGEGISLAVKQAAAAV
SAIVDDTPASYEAAWHRITRDYRLVTRGLVLASTPRAARRAIVPLCALLPTAFRYGVN
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/protein_id="CAB0907.1"
/db_xref="G1:21176"
/db_xref="SPTERBL:006539"
/translation="MYYLLILAVVFERLAELVVAQRNARWSFAQGGKEFGRPHYVVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5546. 6394
/gene="Rv1140"
/note="Rv1140, (MTCI65.07), len: 282. Weak similarity in
/note="Rv1140, (MTCI65.07), len: 282. Weak similarity in
/cterminus to hypothetical E. coli proteins YPRA and YPRB,
possibly membrane-bound. FASTA scores: YPRA_ECOLI
HYPOTHETICAL 24.3 KD PROTEIN (URF 1). - (217 aa) opt:
166: E(): 0.00062; 31.0% identity in 158 aa overlap.
TBparse score is 0.927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILHTALLLGCVVEPWALHRPFIPWLGWPMLAVVVÄSOGLRWWCYKSLGKRWNTRVIVL
PHATLVRRGPYRWMRHPNYVAVVAEGFALPLVHTAWLTALVFTLANATLLTVRLRVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4684. .5184)
/gene="Rv1139c"
complement(4684. .5184)
/gene="Rv1139c"
/note="Rv1139c"
/note="Rv1139c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv1138c, (MTC165.05c), len: 338. Similar to mar
M.tuberculosis hypothetical proteins e.g. TR:P72008
MTCV4C12.35 (412 aa), fasta scores; opt: 89 z-score:
292.1 E(): 4.5e-09, 24.6% identity in 358 aa overlap.
TBparse score is 0.929"
                                                                                                                                                    /note="Rv1137c, (MTCI65.04c), len: 122. unknown"
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5546. .6394
                                                                                                                                                                                                                                              /product="hypothetical protein Rv1137c"
/protein_id="CAB09025.1"
/db_xref="GI:2117175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rv1137c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
/product="hypothetical protein Rv1138c"
/protein_id="CAB09026.1"
/db_xref="G1:2117176"
/db_xref="SPTREMBL:006538"
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/transl_table=11
/product="hypothetical protein Rv1140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3659...3662)
/note="possible RBS, AGGA, for Rv
complement(3671...4687)
/gene="Rv11386"
/gene="Rv11386"
                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:006537"
                                                                                       complement(3286. .3654)
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                                                                                                                     /gene="Rv1137c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 accgettygacyaygtgtettttgaggtgttgacececcagaacggetgcggtetetgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 aacgictggaatgeilggigeyeeggelaceggeggigggicacgegttgaicaaceaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttgacycccaaqcraycyayyaaqaartggycggcargctgtgctgcgcgctggccaacc
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(bases 1 to 14953)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpcutter,L., White,O.,
Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Hatt,D., Hickey,E.,
Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Kheuri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
     | ||||
|-----TCTGGCA 14868
                                                                       14867 TIGITIGAGGCGCTAGCGTTGGCGTTGGCGTTGGCGTTAGCTTCCCCGGCG 14808
                                                                                                                                              '(bases I to 14953)
Fleischmann, D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, T., DeBoy, R., Dodson, R., Gwinn, M., Ermolaeva, M., Salzbergy, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Direct Submission
Submitted (25-ARR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                     atcttcgaccacggcacacccctggcgctgtatcacaccaaacgcctagcctccccggcc 1080
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                                                                                                                            cagoggateatgetgttcgccaacgaccgcggctgcaccaaacccggctgtgacgcaccg
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;

    14953
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AUTHORS
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JOURNAL
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PLOPVVAVVVOGPTVGGOSIALACIDEVLASDREFKILAHTWGLMPDGGASA I VOAA
I GRI RAMHMA ILLPPVYAALALENGI VSAVY PAADFDAEVDK I SKILAGPALA I AKT
KNA I NAATL TELAPTI LRELDGGALLLETDDFAEGATFAFQORRPMFTGK
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ELALKLJRAKADVL BGYRPGYTERLGLGPECGAKNDRLI YA RWTGWGOTGPRSQQAG
HID INY ISLNGI LLHA IGRORPRYPPILLYGDFGGGSMFLLVGI LAALIMEKYSSCKGOV
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PUFY AAMLAGLGLDAAELP PONDRAKWPELRALITEAFASHDRDHWGAVFANSIJACVT
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PID:1787660; identified by sequence similarity; putative"
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PID:1787660; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ttgacgcccaaqccagcgaggaaqaactgggcggcacgctgtgctgcgctggccaacc
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                                                                                                                                                                                                                                                                                                            Pred. No. 1.7e-86;
0; Mismatches 385; Indels
                                                                                                              putative"
                                                                                                              /note="identified by Glimmer2;
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                                                                                                                                                                                                                                                                                          Score 698;
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                                                                                           /gene="MT1183"
                                                                                                                                                                                                                                                                                      Query Match 50.1%;
Best i.cal Similarity 70.4%;
Matches 974; Conservative
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ATFWPRLAGACHTHRHTERAILDAGFVVDSSRREWAPPAWVPLPVSELALGRAHRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTTSQYAAVAAAHSVDPDRWQAEFSAVLDRIAPRFARHQPLRHA
GELMAGWVSGLDRKNCWTIAEHRGDTTPMGCSICWHGPAGTPTMSVTICVTIAIDRWR
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SKTYVDILVGGTRVLELGAERIAKTEPIGEERGVIINTASVAAFDGQIGQAAYSASK
GGVVGATLEPTARDLASKLIRVVTIARGLEDTPLLASLPAEARASLGQQVPHFSRLGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5395. 7739

Agene—Whili9.1"

/note—This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by dilmmerz; putative; conserved hypothetical protein, authentic frameshift.

7872. 8522

7872. 8522

/gene—Whil80"

/gene—Whil80"
                                                                                                                       "WWH
                                                                                                                       family
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/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                   /gene="MT1178"
/note="identified by Glimmer2; putative"
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                                                                                                                       protein
                                                                                                                                               /transl_table=11
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                                                                                                                       by match to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MT1182"
complement(9000. .9302)
                                                                                                                                                                                                                                                                                                                                      complement(5008. .5163)
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                                                                                                                         /note="identified
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/trans1_table=11
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8614. .8916
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                                                                                                                                             /codon_start=1
                                                                                     4128. .4880
/gene="MT1177"
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I (bases 1 to 33100)

S Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekala, F., Badcock, R., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Squares, S., Squares, S., Staten, S., Staten, S., Barrell, B.G.

Berrell, B.G.

Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTCY9F9 33100 bp DNA BCT 03-AUG-2001
Mycobacterium tuberculosis H37Rv complete genome; segment 87/162.
284498.1 GI:3261701
atccgcatgaccagcccaccaccactactccccgcaagcgggaggtaccccaggcg 1020
                                                                                                                                                                          9676 ATCGGATGGGGAGCCAGCCACCACTA-----TCTGGCA 9641
                                                                                                                                                                                                                   1021 atcttcgaccacggcacaccctggcgctgtatcacaccaaacgcctagcctccccggcc 1080
                                                           cagoggatcatgctgttcgccaacgaccgcggctgcaccaaacccggctgtgacgcaccg 1140
                                                                                                                                                                                                                                                                                           901 caaaccggcgccggcaagggcttcaccggcggcgccctgctacccatggccgutgtg 960
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                                                                                                                                                                                                                                   Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence
Nature. 393 (6685), 537-544 (1998)
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Parkhill, J.
Direct Submission
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VERSION
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TITLE
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MTCY9F9
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dvallable on the World Wide web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes inplemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/axpected third position G + C. GAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg., 9tg., or ttg) which is preceded by an upstream ribosome codon): If this cannot be identified we choose the most upstream codon.
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/db_xref="G1: H806240"
/d
cubmilted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1806198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        penicillin binding proteins and eg DAC_STRSQ P1555
d-alanyl-d-alanine carboxypeptidase (406 aa), fasta
scores, opt. 382,E(): 3.1e-17, (28.0% identity in 379 aa
overlap); containsPS00013 Prokaryotic membrane lipoprotein
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/organism-"Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
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/organism~"Mycobacterium tuberculosis H37Rv"
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265. .1380
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Acyl-CoA synthase similar to eg Y06J_MYCTU 010976
hypothetical 67.9 kd protein cy338.19 (626 aa), fasta
scores, opt: 945, E(): 0, (39.8% identity in 598 aa
overlap), also G1171128 SAFRAMYCIN MX1 SYNTHETANSE B(1770
aa), opt: 845, E(): 0, (37.4% identity in 593 aa overlap)
also MTCX19G5.07 (36.9% identity in 593 aa overlap)
similar to RV3801c, (637 aa, 47.1% identity in 612 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT.P97175"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aa. Unknown"
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Agene="Rv1926c"
Complement(5155 ..5634)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2748. .3128)
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3285. .5147
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/gene="Rv1927"
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WPRRGLRSLITTTGDLVPFTPLEVWLTARAGAHTRAGGTWWVPNEHRPSRHITTHSPRAR
WHIDELIDASSVQPTGDRIRALFSPGVHARRGRFCWVQ"
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/genew Rv1928c."
/note-"Rv1928c."
/note-"Rv2002, Rv2069, Rv2766c.
/note-"Rv1936o.
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/note-"Rv
/note="Rv1927, (MTCY00F9.37c), len: 257 aa, Slight similarity with YQJF_BACSU P54543 hypothetical 23.9 kd protein in glng- (209 aa), fasta scores, opt: 230, E(): 2.8e-08, (28.0% identity in 164 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22248 CGCGGGTGCTCCATCTCAAGTGCGATGCGTTGACCACCCCGGAATTGCTGGCCTGTTTGC 22307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGTCGACACGCGCGAGGAGATCTCCGCGGCGTTGGATGCTACCACGCCTCGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttgacgcccaagccagcgaggaagaactgggcacgctgtgctgcggctggccaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 aacgccagggcctgatcggcgaggcgcacgtcaaagtgattcgccctttttcgcccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ctgcccgccgcggtggatgtgtccacccgccaggccgccgaagccgacctggccggcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caccegaeggegaecteacegaeaegegeeegeaaegegeateaeeetgage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 aaccagcaatacgacggcatgtcacggctaagtggctacctgacccccaagcgcgggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.1%; Score 683.6; DB 1; Length 33100; llarity 69.7%; Pred. No. 1.1e-84; Conservative 0; Mismatches 394; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6648. .7415)
/gene="Rv1928c"
                                                                                                                                                                                    /codon_start=1
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JOURNAL
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                                                    AUTHORS
                                            REFERENCE
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                TITLE
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                                                                                                                                                                                  13087 GAAGCCGCCACCGGCAAGGGGTAACCGGTGGTGGGTTCGCGGGTGCCGATGTCGGACCTT 23146
                                                                                                                                                                                                                              23242
                                                                                                                                                                                                                                                                                                                                         23362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynabacterineae; Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex.

1 (bases 1 to 14179)

Fleischmann, R.D., Alland, D., Elsen, J.A., Carpenter, L., White, O. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
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                                     atcogratgaccagccaccaccactactccccgcaagcgggaggtaccccaggcg 1020
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of 280 of the
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                                                                                                                                                                         caaaccggcgccggcaagggcttcaccggcggcggcaccctgctacccatggccgatgtg
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                                                                acccggtcatcgacaccacccgatgcgccgccatcgaccgcgacaccgcagacaccfcaga
                                                                                                                                     Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria: Actinobacteridae;
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Mycobacterium tuberculosis CDC1551,
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AE007053 AE000516
AE007053.1 GI:13881639
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KEYWORDS
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TDPRVRDGLAWCYARVQIMRYRGYRDLTLALTGRPPGAEAAITKVTWSEYFRRYTDLA
VEILGLEALGPRGDGGARLVPEAGTPNSPACWMDELLYARAATIYAGSSQIORNVI
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HWRRALAGACLVAVSWPTEYXGGLSPMEQVVLAEEFARAGAPERAENDLFGIDLLGN
TLIALGSEAQKRHFLPRILSGEHRWCQGFSEPEAGSDLASVRTRGVLDGDEWYINGHK
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VIJDVARVLLAAEMLGGAEACLDLAVOYAGRRTQEDRPIGSRQAVKHACADMMI EIDAT
KATVMFAAMSAANGDELGTVAPLAKAQTAETFVLCAGSALQ I HGA I AFTWEHDLHLYY
KRAKTTEALFGSSARNRALLAERAGLVKA"
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Thieldaling physpherical Gatelyeth I arabigraith i pfaatyfa i bai lrhoddo
krrillagilitean i citlayschdyasattyrayrrdorpaliterctiyllhohyadlfy
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KSVLLNIFPSVDTPVCATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVM
PASAFKDSFGEDYGVTIADGFMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAAL
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
Unpublished
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Pleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Ermolaeva, M., Hickey, E., Rolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
Incation/Qualifiers
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PID:1787584 PID:1931625; identified by sequence
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/gene="MT1984"
/note="similar to GB:X61931 PID:47382; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDC1551
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/strain="CDC1551"
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/transl_table=11
product=acyl-CoA dehydrogenase,
/protein_id="AAK46256.1"
/db_xref="G1:13881642"
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/protein_id="AAK46254.1"
/db_xref="GI:13881640"
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/gene="MT1984"
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/gene-"MT1983"
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/gene="MT1983"
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91. .588
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RVWYQDYFAVQDG I ITEI EEDLRGMLLGLTYTVSGEGMMAATKAAVIJAGVDLESMDP I
DVI RAGPLCMAEGARI,KDAFVYPETMPAWFTEADLDFYTGEFERSGFGGPL,SFYHNI D
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MAASSFTSVSVDPPLVSTCVQNCSTTWPKLRDRPRLGVSVLAEGHDAACMSLSRKEGN
RFAGVFWSELSSGGVVJAGAGAMLDCRPYAEJPAGDHLJALLETCAVRADPETPPLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="3,4-dihydroxy-2-butanone-4-phosphate
synthase/CTP cyclohydrolase 11"
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/translation="MKTTDVRVRRAITAMAGGHAVVLTGDPNGDGYLVFAAQAATPRL
       /translation="MSQVHRILNCRGTRIHAVADSPPDQQGPLVVLLHGFPESWYSWR
                                  HQTPALAGAGYRVVATDQRGYGRSSKYRVQKAYRIKELVGDVVGVLDSYGAEQAFVVG
HDWGAPVAWTFAWLHPDRCAGVVGISVPFAGRGVIGLPGSPFGERRPSDYHLELAGPG
                                                                                                                                                                                      NDWHDLADQQCKPLTPPALFIGGQYDVGTIWGAQAIERAHEVMPNYRCTHMIADVGHW
TQQEAPEETNRLLLDFLGGIRP"
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MAAASATSVAADIVQHQVPQVQAQDOVUGRRAPAAADIVGHGETASAASASASSASSASSADIVARVERERAAALICETV
SIVDRVQMAHHAESVERAVEBGLAMVS1GELVAYRRR EPQVVRFTATI.PTWAGASR
V1GFRUVYDLGEHLAV1VGAVGAGVPVPLHVH1ECLTGDVFGSTACRCGEELNGALAR
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/codon_start*!
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/protein_id-"AAK46261...
/db_xref="G1:13881647"
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/wene-"MT1989"
8813. .9328
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/qene-"MT1990"
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/qene-"MT1989"
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PDQHPSYRCNGATFGGVESRNRQEWHYYFENTKRWRNLRK1T1AQVHGAVLSAG1MLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVEEGALÄSGRTPDRRDWRLVREVLVAETDEGAFRYAVDGTWGRAMREYVLPFFRWFG
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LSATLAMAGSLDADVAHPVLLYGVERFEDLCLETERRRGVGRLEHVVVARPDP
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GVAVDNGDADGGDGLQVVPAEFVVDASGKNTRVPFFLERLGVGAPEAEGDIINCFYST
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RERRAFADLMPSPVIGENIDGLEPASPIYNRRYPMLRLRYEKKRNLPRALLAVGDAY
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VTGDGVVTAVELVSPSTAILRVDTSGMAGALRYRAGQFAQIJQVPGTNVWRNYSYAHPA
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/product="enoyl-CoA hydratase/isomerase
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Copyright (c) 1993 - 2000 Compugen Ltd.
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length: 2000000000
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Post-processing:

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Total number of

Searched:

Minimum DB seq Maximum DB seq

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Scoring table:

Mahairas GG, Stover CK; WPI; 1996-393419/39

455 455 455 396 396

Score 1202.4

Result

94.4 89.8 89.4 87.4

Human colon cancer Probe #11714 for g Probe #15750 used Probe #7457 used t Probe #2526 for ge

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This DNA sequence comprises Mycobacterium bovis BCG deletion
sequence BCGdelta3. A specific genetic deletion of this region
ceaults in an avivalence phenotype of the mycobacterium. 2 other
celetion regions (see AA713535 and AA733536) have also been detected.
Identification involved screening a BCG cosmid library with a
redicible deprobe obtained following DNA subtraction between
cridicabeled probe obtained following DNA subtraction between
virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
The deletions provide useful markers for the identification of an
avirulent, or a virulent, mycobacterial phenotype. Determination
of avirulence requires the detection of the presence or absence of
the deletion; the deletions are detected either by detecting the
presence or absence of deletion junctions (see AA733538-46), or by
detecting the presence or absence of the sequences contained within
the deletion. Deletion polypeptides are used as components of
Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological assays and in vaccines
                                                                                                            English.
                                                                                                            Example 1; Fig 3; 66pp;
                                                       bacterial infection
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Score 1202.4; DB 17; Pred. No. 5e-212; 86.3**%**; 95.7**%**; Similarity

5;

246 305 186 364 143 tggacgaggtgtcttttgaggtgttgaccacccagaacggctgcggtctctggaacgtc 126 323 cgggtagccgcgaacggattgtcgaggtctttgatgcgctggatgccgagctggaccgct 66 Gaps cgaatagccgggaggaggttgtcgaggtctttgatgcgctggatgccgagctggaccgct cccaagccagcgaggaagaactgggcggcacgctgtgctgcgcgctggccaaccggttac gcatcaccaagcccgacgcccggcgcatcgccgacgccgacgccgatctcggacctcgttgcccgccgcggtggatgtgtc--acccgccaggccgccgaagccgacctggccggcaa accgctcaaatatcgtcccgacgagctggcccgctacgcccagcgggtcatggactggct acaccccgacggcgacctcaccgacaccgaacgcgcccgcaaacgcggcatcacctgay 624 acaccccgacggcgacctcaccgaccccgaacgcgcccgcaaacgcggcatcacctgag tgcccgccgcggtggatgtgtccaaacccgccaggccgccgaagcccgacctggccgcaa agccgctcaatatcgtcccgacgagctggcccgctacgcccagcgggtcatggactggct Length 12412; 7; 51; Indels 0; Mismatches Conservative Query Match Best Local Simi Matches 1290; 444 422 504 480 564 540 900 127 264 306 384 365 7 84 67 204 187 247 324 g ò qq à g ò qq á g ò g ò qq ò a ò a ò g ò õ

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caccccggtcatcgacaccaccrcgatgcggccgccatcgaccgcgacacccgcagcca
                                                                           ageceaacycaaceucgaegggetgetggeeggggetgegegegetgategeetecyggaa
                                                                                     gcaaaccggcgccyycaagggcttcaccygcygcggcaccctgctacccatggccyatgt
                                      caccccgg tcatcgacaccacccccgatgcggccgccatcgaccgcgacacccgcaycca
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M. tuberculosis cellular uptake gene region.
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                              vaccine;
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                     The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydroj hobic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with list carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                       acaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaacc
                                                                                                                                                                                                                                                                                                                                                                                        accteaccgacaccgaacgcgccgcaaacgcggcatcaccctgagcaaccaguadlacg
                                                                                   DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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0
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                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                    Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                              32.7%; Score 455; DB 16;
100.0%; Pred. No. 4.1e-75;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        794 acgacgggctgctggccgggctgcgcgctgatc 828
                                                                                                                        Claim 2; Page 9-11; 46pp; English
                          (CORR ) CORNELL RES FOUND INC
        93US-0118442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT33656 standard; DNA; 1535
                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 455; Conservative
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                                                          WPI; 1995-115442/15.
P-PSDB; AAR71931.
        02-SEP-1993;
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                                          Riley LW;
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A DNA molecule (AAT3465b) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The encoded protein sequence is given in AAM02301. The DNA was obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coll strains for HeLa cellminsus or clones. The DNA includes 2 separate coding regions (see also AAT34657-58) confine for the cell entry (AAM02302) and macrophage survival (AAM02301) proteins. He can be used to produce the cellular uptake proteins used as vaccines of to facilitate uptake of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 galoggogaygogrargloaaaqigatlogooottiltogooocacetgooogoogg 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 gicccgacgagetggcccgctacgcccagcgggtcatggactggctacacccgacggcu
Cellular uptake; cell entry; macrophage; passive immunisation;
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                                                                                                                                                                                                                                                                                                                                         protein
                                                                            Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.7%; Score 455; DB 17; ilarity 100.0%; Pred. No. 4.1e-75; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 /product= macrophage survival
                                                                                                                                                                                                                                    entry protein
                                                                                                                               Loration/Qualitiers
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886..1535
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/label- ORF-1
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/label- ORF-2
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                               gene therapy; ds.
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Claim 7; Page
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                                            to enhance uptake of in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to
          1067 acggcatgtcacggctaagtggctacctgacccccaagcggggcgacctttgaagccg
                                                                               acaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaacc
                                  tgctagccaaactggccgcccccggcgcgaccaaccccgacgaccacaccccggtcatcg
tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                        DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis DNA - confers ability therapeutic agents e.g. antibiotics, also useful
                                                                                                                                                                                                                                                                                               Cellular uptake protein; vaccine; infection; ds
                                                                                                                                      /note= "stop codon not given"
                                                                                                                         794 acgacgggctggccgggctgcgcgctgatc 828
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                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
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Length 1535;

Score 455; DB 19; Pred. No. 4.1e-75;

32.7%;

Query Match 32.7 Best Local Similarity 100. Matches 455; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA molecule (AAT33558) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT33556) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protect
acctcaccyacaccyaacycgcccychaacycygcatcaccctgagcaaccagcaatacy
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                                                        tggatgtgtccaccccaggccgccgaagccgacctggccggcaaagccgctcaatate
                                                                                                              glecegaeqagelyyceeqetaegeecagegagtealggaelggetacaeceegaeggeg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to p mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular uptake; cell entry; macrophage survival; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis strain H37Ra (AEC 25177)
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                                                                                                                                433 gtggatgtgtccacccgccaggccgcagaccgacctggccggcaagccgctcaatat
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                                                                    Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                             Score 396; DB 17;
Pred. No. 2.6e-64;
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                                                                                                                                                                                                                                                                                                                                             cacgacgggctgctggccgggctgcgcgcgctgatc 828
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/note= "stop codon not given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which conters on M. tuberculosis an ability to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-reoplastic agents. Antibodies raised against it can be used to Lreat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
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                                                                                                                                                                                                                                                   um tuberculosis DNA - confers ability agents e.g. antibiotics, also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 396; DB 19;
Pred. No. 2.6e-64;
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                                                                                           WPI; 1998-145620/13.
Riley LW;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Avermectin aglycone synthase DNA and proteins encoded by all or part of it for the production of avermectin and its derivatives for drug and
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Location/Qualifiers
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ilarity 45.0%; Pred. No. 5.2e-09;
Conservative 0; Mismatches 631;
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581 aacgcggcatcaccctgagcaaccagcaatacgacggcatgtcacggctaaglgyctacc

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21842 cactgetecageagececgtaegeceagecegeeetettegeettecaggtegeeetee 21901
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detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                    cgaccaaccccgacgaccacaccccgqtcalcgacaccaccccgatgcggccgcratcg
                                                                                                                                      accgcggctgcacraaacccggctgtyacgcaccggcctaccacaggccaagcccacg
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                                                                                                                                                                                         accycyanacceyragecaagerraaryraacgacyggetgetggeegggetyrqey
                                                                                                                                                                                                                       22022 teacecaacgegeraceteatgeaaaceatgeeeeeggeaceatgaceaceteeaca
                                                                                                                                                                                                                                                          c-----gotyategeotecyggaaactyggecaacaacaacggtottecegtetega
                                                                                                                                                                                                                                                                                                                                                             22142 ceateaanacennacetrectryteatragonggeaengeecacegteeaacanatra
                                                                                                                                                                                                                                                                                                                                                                                                                                 22202 ccaccetetgccaaraacaaggoat.caaaaaccaaaaaceteeccaaccaacgcettee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actactccccgcadycggggggtaccccagggggtcttcgaccacggcacccctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22262 actococcaacoascocatoutoascoaactocacoagoacacocaaaccotoacot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1046 egetgtateacaceaaacgeetageeteeeeggeecayeggateatgetgttegeeaaeg
                                                  641 tgaccccccaagcgcgggccacctttgaagccgtgctagccaaactggccgccccggcg
                                                                                                                                                                                                                                                                                                                              872 tegtggteaceaceaecelgaeegaeetge----aaareggegeeggeaagggettea
                                                                                                                                                                                                                                                                                                                                                                                                  coggodgoggoarmitantachalpatotatatrogoatgaocagocacgoncam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            teacegeetygaceageaceggacycacegacate...accgagetgacectggeetgeg
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12512 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynuclectide sequences given in AAZ12312 to AAZ17779. The polynuclectides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profilling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides and be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). "he polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                    Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 A; 577 C; 27 G; 22 T; 669 other;
                                                                                                                                                                                                                                                                                                                                                                                          Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide analogues and antagonists.
                                                                                                                         98US-0072910.
98US-0075954.
98US-0080114.
                                                            99WO-US01619.
                                                                                                         9990800-S086
                                                                                                                                                                                          98US-0080515
                                                                                                                                                                                                                                                                                  Crkvenjakov R, Dickacu. .
کیار Garcia PD, کیدا
                                                                                                                                                                                                                                       CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1337 BP;
                                                                                                                                                                                                                                     (CHIR ) CHIRON (HYSE-) HYSEQ I
                                                               28-JAN-1999;
                                                                                                                              28-JAN-1998;
                                                                                                                                                                                          03-APR-1998;
                                                                                                         03-APR-1998;
                                                                                                                                                  24-FEB-1998;
                                                                                                                                                                        31-MAR-1998;
                    05-AUG-1999
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gaggcgcacgtcaaagtgattcgcgccctttttcgcccacctgcccgccgcggtggatgt 440 cgagetggecegetaegeecagegggteatggaetggetaeaeecegaeggegaeeteae 560 gacgocgcccggcgcatcgccgacgccgccgatctcggacctcgtcgagcactcaccggt 320 gaaccgctagccccacagttgaccgccaccgcccacgcccaacgccagggcctgatcggc gtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatatcgtcccga 6.4%; Score 89.8; DB 20; Length 1337; .larity 23.4%; Pred. No. 3.3e-08; Conservative 0; Mismatches 860; Indels 11; Query Match Best Local Similarity Matches 266; Conserv 266; 166 226 381 286 321 501 q g g ò οy ò

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agccacgcccaccactactcccccgcaagcgggaggtacccccaggcgatcttcgaccac 1032 caageeeaeracgicacegeetigaeeageaeeggaegeaeggaea---teaeegagetg 1209 1126 nnconcompagnation conconcumum conconnon no national conconconconcus 1185 accoacyyceacancyaatyyetaceaceaceceaceteyaceacygecaaceegeace 1329 сиссепсинененниевпесиненнениевписивненспенсисиспесссописсине 1125 705 cgacaccgaacgcgcccgcaaacgcggcatcaccctgaycaaccagcaatacgacggcat 620 Streptomyces avermitilis avermectin polyketide synthase modules 1+2. 1330 aacaccttccaccaccccgaacgattcctccacaagacgacgacgacaaaccc 1386 glyctagecaaacluyccqccccggcgcgaccaacccgacgaccacacccggtcatc 1033 ggcacaccentggegetglateacaccaaacgectagecteeeeggeeeageggateatg noncececenencenations 766 nnocancenneenecuecuenennnnnnneecencenennnnenneneceeneneene cnnnncncncncccnccnnnnnnncncnccnnncncnccnnnccnccnnccn ctgttcgccaacgaccgcggctgcaccaaacccggctgtgacgcaccggcctaccacagc accetygeer) gequeeccaccaneryant egergaaaaaggetygaccaccaccaccac cecennnnnnnnnecenececenececenececenececececececececenecen gacaccaccccqatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaac cacgacgggctgccggggctgcggcgctgatcgcctccgggaaactgggccaacac ggcaagggcttcaccggcggcgcaccctgctacccatggccgatgtgatccgcatgacc gtcacggc----taagtgqctacctqacccccaagcggggccacctttgaagco ກວວດຕາກດຍຕາກຄວາມຕາກຕາກຕາກຕາກຕາກກອດຕາກກອດຕາກກາກຄວາມກອດຕາມກາກຄວາມຕາມກອດຕາມຕາມກອດຕາມການຕາມກອດຕາມການຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດຕາມກອດການການກອດການກອດການກອດການກອດການການກອດການກອດການກອດການກອດການກອດການກອດກ nennnncennnnnconcennnnnnnnnnceeenenneeneeneenennnnet Polyketide synthase; avermectin; insecticide; BP. AA258381 standard; DNA; 12381 (first entry) Streptomyces avermitilis. 23-MAY-2000 AA778381; 621 673 826 1093 1006 1153 1066 1210 1270 1186 261 526 586 733 793 907 913 973 946 AAZ58381 ID AAZ g Q ô g ò Ω δý qq QQ δλ Ω ογ Db g Dp qq qq òγ ò Ω οy Db δy ò òγ ó ò

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us-09-785-904-1.rng

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                                                                                                                                                                                                                                                                                                    polylinker site in
loop sequence, for
                                                                                                                                                                                                                Stutzman-Engwall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12381 BP; 1884 A; 4561 C; 4005 G; 1931 T; 0 other;
                                                                                                                                                                                                                                                                                                 Mutated Type I polyketide synthase containing a extension module for replacement of a reductive producing polyketides, e.g. Bl avermectin
                                                                                                                                                                                                                Staunton J,
                                                                                                                                                                                                                                                                                                                                                                        Disciosure; Fig 7a-f; 75pp; English
                                                                                                                                                            BIOTICA TECHNOLOGY LTD.
                                                                                                                                                                                                               Leadlay PF,
                                                                                       99WO-GB02158
                                                                                                                         98GB-0014622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       avermectins are claimed
                                                                                                                                                                                                                                                                 WPI; 2000-182117/16.
                                                                                                                                                                                                               Kellenberger JL,
                                                                                                                                                                             (PFIZ ) PFIZER
                WO200001827-A2
                                                                                                                                                                                                                                 McArthur HAI;
                                                                                       06-JUL-1999;
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                                                  13-JAN-2000
                                                                                                                                                            (BIOT-)
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5; 9048 cggcaaagccgctcaatatcgtcccgacgagctggcccgctacgcccagcgggtcalgga 8809 actcaacgacatctgcacccacctcgacccccacctcgaccaccccctcctccccct cacccaaaacgacaacgacaacgaggacgcggccgcactgctccagcagacccgctacgc ccagecegecetettegeettecaggtegeettecacegeetceteacegacggetacea 8989 catcaccccactactacgccggacactccctcggcgaaatcaccgccgccactcgc 774 cagecaageccaaegeaaceaegaeggetgetggeegggetgeeggegegegetgategete ctggctacacccgacggcgacctcaccgacaccgaacgcgcccgcaaacgcggcatcac cctgagcaaccagcaatacgacggcatgtcacggctaagtggctacctgaccccaagc 654 gegggccacctttgaagccgtgctagccaaactggccgccccggcggcgaccaacccga 9049 eggeatecteacecteacegaegecaceaceteateaceaaegegecacetratgea 714 cgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 6.4%; Score 89.4; DB 21; Length 12481; Similarity 44.6%; Pred. No. 4.2e-08; 77; Conservative 0; Mismatches 536; Indels 6; Query Match Best Local Simi Matches 437; 474 534 8929 414 8869 594 à q ò g ð a g g ò ò

auccatgococoggicaccatgaccacctccacaccccccccccccccccatcarccard 9168

1190 occodagogate Legaceacegeacecentggegetgtateacaceaaegentage 1070 FK-520: polyketide synthase; PKS; gene cluster; immunosuppressant; immunophilin; FK-506 binding protein; polyketide compound; uveitis; transplant rejection; graft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; trammatic spinal cord; brain injury; peripheral neuropathy; ss. 9649 caaceteyeeaaaaneaceaceaceyeelyyeaceecaceactacacccaccaccacaaca 9708 1248 aggetggaceacecacaacaacaceceggecacacegaatggetaecaceceacet cotcaccycccacyaaaacgacctcyccatcyccyccatcaacaccccacctccctcy 9229 calcagoggeaccurcacacacoglocacacacacacacacaacaacaagaal ggnegatglyalenyealgaceayeraegeeeaceactacteceeegeaagegggaggla ctecceggeceagegateatyelgtleyceaacgaeeggetgeaceaaaeeggetg Candyacaadacccaacaactactcacccccaactagacccaacaagcccq 1131 igacycarrogertucrarageraderrangrenegicaeegeeiggaeeageaerggarg cgggaaactgggccaacacaacggtcttcccgtctcgatcgtggtcaccaccc---t Caaaaccaaaacceteceaaceaaceaacecaaceceaaceceaaceceatect caaccaaetecannugeacaeeecaaaeeeteaeetaenaeecaeeeeeeeeeeteat caacaccylegaetacgecaecaeceaacetecaecaacaeggeyteaecta caccyacato---arcyayotgacctygcctycggcccgacaaccgactcgccgaaaa cgaccacyyccaarrecycaccaacarctccaccaccccgaacgattcctccacaacca gacegacetgeaaaneggegeeygeaagggetteaeeggeggeggeaceetgetaeeeat categateteggaceegacacceteaceaceteaceaceacaacateceeaacac Nucleotide sequence of a fragment of the FK-520 PKS gene cluster. /\*tag= a /note= "no termination codon given" Location/Qualifiers . : 1368 agacgacgacgacaaccc 1386 9709 acccacacccacaccac 9727 AAA14663 standard; PNA; 4466 99WO-US22886 (linst cotty) hygroscopicus 9..4454 /\*tag= WO200020601-A2 Synthetic. Streptomyces 08-AUG-2000 01-OCT-1999; 13-APR-2000 AAA1466 1; 9169 891 951 9289 9349 1071 9409 9529 6886 RESULT 10 6946 1191 1308 AAA14664 qq ò ò qq ò Op ò Db δ qq ŏ QQ ò q ò d ŏ Dp 

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The prescut sequence represents an NheII-XhoII fragment that encodes module 8 of te FK-520 polyketide synthase (PKS) gene cluster with the endoqueous acyltransferase (AT) domain replaced by the AT domain of endogenous acyltransferase (AT) domain replaced by the AT domain of module 12 of the rapamycin PKS (which is specific for malonyl CoA).

FK-506 is a potent immunosuppressants, and acts through initial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide compounds. The polyketide compounds can be used as immunosuppressants to prevent or treat transplant rejection, graft-versus-host disease or uveitis. They can also be used for treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease, multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurine outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and continued repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, altoke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and vertical vertica
                                                                                                                                                                                                                                                                                                                                                              ed polyketide synthase nucleic acid and polyketide compounds, treating e.g. transplant rejection, uveitis, multiple Alzheimer's disease, Parkinson's disease, stroke, or
                                                                                                                                                                                                                   Wu K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 82-85; 126pp; English.
                                                                                                                                                                                                                   Santi
                                                                                                                                                                                                                                                                                                                                                                    isolated polyketide synthase
                                                                                                                                                BIOSCIENCES INC
                         99US-0102748.
99US-0123810.
99US-0139650.
                                                                                                                                                                                                             Chu D, Khosla C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reterinary applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral neuropathy
                                                                                                                                                                                                                                                                    WPI; 2000-317716/27.
                                                                                                                                                                                                                                                                                                       P-PSDB; AAY84727
                                                                                                                                                      (KOSA-) KOSAN
                                                         11-MAR-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                             Reeves C,
                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                 useful
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3784 3605 gcaacaccacctcaccaccaccgaccacacctcatcgtccacaccaccaccgacccgc 3664 catggccgatgtgatccgcatgaccagccacgccaccactactccccgcaagcgggag 1007 gtacccccaggcgatcttcgaccacggcacaccctggcgctgtatcacaccaaacgcct 1067 agceteceeggeecageggateatgetgttegeeaacgaeeggegetgeaceaaaeeegg 1127 3545 cgaccccgaggacatacccaccgcgcccacacccgcgcccacccgcgtcctgaccgcct 3604 caccaccaccccaccaccaccaccccctcaaccccgaacacgccatcatcatcaccgg 3904 egectecgggaaactgggecaacacaacggtetteegtetegategtggteaceacae 887 3725 ceteategaaacegaceacececeacacececetegacecaactegecacetega 3665 eggegecacegicaceggecteacegeacegeceagaacgaacaceceacegeateeg cctgaccgacctgcaaaccggcgccggcaagggcttcaccggcggcggcaccctgctacc ctgtgacgcaccggcctaccacagccaagcccaccacgtcaccgcctggaccagcaccgg 0; DB 21; Length 4466; Indels Mismatches 296: Score 87.4; DB 21 Pred. No. 9.5e-08; .. 6.3%; ilarity 47.2%; Conservative Query Match Best Local Similarity Matches 265; Conserv 828 888 948 1008 1068 1128 3845

g ò a ò g ò q οy qq acgcaccgacatcaccgagctgaccctggcctgcggccccgacaaccgactcgccgaaaa 1247

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The present sequence represents an AvrII-XhoII fragment that encodes module 8 of te FK-520 polyketide synthase (PKS) gene cluster with the endogenous acyltransferase (AT) domain replaced by the AT domain of module 12 of the rapamycin PKS (which is specific for malonyl units). FK-506 is a potent immunosuppressants, and acts through intial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polyketide synthase nucleic acid and polyketide compounds, useful for treating e.g. transplant rejection, uveitis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or perlipheral neuropathy
                                                                               immunophilin; FK-506 binding protein; polyketide compound; uveitis; transplant rejection; qraft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss.
cgaccaeggecaacregeacraacacettecaccaerregaacgattectecacaacea
                                cototocoggaececcocoggaecgaececcoggaececcaecetecectgegaecetegg
                                                                                                                                                                                                                                                                                                                                                                          gene cluster; immunosuppressant;
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/mote~ "no termination codon given"
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Sequence 4466 BP; 634 A; 1796 C; 1433 G; 603 T; 0 other;

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be used as immunosuppressants to
                             uveitis. They can also be used for treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease, multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurite outgrowth in NGF-treated POI2 cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and sciatic nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
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                       prevent or treat transplant rejection, graft-versus-host disease or
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                                                                                                                                                                                                                                                                                                                                               Score 87.4; DB 21;
Pred. No. 9.5e-08;
O; Mismatches 296;
  can
  compounds. The polyketide compounds
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module 8 of the FK-520 polyketide synthase (PKS) gene cluster with the cudogenous acyltranslerase (AT) domain replaced by the AT domain of module 13 of the rapamycin PKS (which is specific for methylmalonyl CoA). FK-506 is a potent immunosuppressure, and acts through initial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The moticie acids are used for producino polyketide compounds can be used as immunosuppressarts to prevent or treat transplant rejection, graft-versus-host disease or uveilts. They can also be used to treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease.

Multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurine cutyprowth in NGF-treated PC12 cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and scitc nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheiner's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
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immunophilin; FK-506 binding protein; polyketide compound; uveitis; transplant rejection; graft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; tranmatic spinal cord; brain injury; peripheral neuropathy; ss.
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3806 cctcatcgaaaccgaccaccacacccccctcccctggcccaactcgccacctcga
                                                                                                                                  1188 acgcaccgacatcaccgagctgaccctgggcctgcggcccgacaaccgactcgccgaaaa
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/note= "no termination codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene cluster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
9..4559
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyketide synthase; PKS;
                                                                                                                                                                                                                                                                                                                       ВЪ
                                                                                                                                                                                                                                                                                                                                                                                             AAA14662 standard; DNA; 4571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0102748.
99US-0123810.
99US-0139650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US22886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hygroscopicus
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral neuropathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200020601-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1998;
11-MAR-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   AAA14662;
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module 8 of to FK-520 polyketide synthase (PKS) gene cluster with the endogenous acyltransferase (AT) domain replaced by the AT domain of module 13 of the rapamycin PKS (which is specific for methylmalonyl CoA). FK-506 is a potent immunosuppressants, and acts through initial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide compounds can be used as immunosuppressants to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and in intect animals, they promote regrowth of damaged facial and sciatic nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. parkinson's disease, Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
                                                                                                                                                                                                                           New isolated polyketide synthase nucleic acid and polyketide compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent or treat transplant rejection, graft-versus-host disease or uveitis. They can also be used for treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease, multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurite outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 egecteceqqqaaactyggccaacacaacggtettecegtetegategtggtcaccaccac 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents an AvrII-XhoII fragment that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1068 agcotcoccygococayoggateatgetgttegceaacgacegeggetgeaceaaaceegg
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                                                                                                                                                                                                                                                              useful for Lreating e.g. transplant rejection, uveitis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4571;
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Pred. No. 9.5e-08;
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                                                              Santi
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(KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.38;
                                                           Khosla C,
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                                                                                                                                                                                                                                                                                                                             peripheral neuropathy
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es 265; Conserv
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                                                           Reeves C,
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Matches
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/*tag= r
/note= "acyltransferase domain (AT) 6"
complement (17820..19053)
                                                                                                            /*tag~ q
/note- "dehydratase domain (DH) 6"
complement (16587..17820)
                         complement (13761..14394)
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/note= "ACP5"
complement (19464..20097)
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/note= "DH5"
complement (21420..22653)
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/note= "fkbB gene"
complement (24163..24373)
                                                                                                 complement (15438..16587)
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/note= "DH4 (inactive)"
complement (26146..27430)
                                                              complement (14517..15294)
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/*tag= af
/note= "DH3 (inactive)"
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complement (28750..28960)
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                                                                                                                                                                                                           complement (19116..19326
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/*tag= ah
/note= "KS3"
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/note= "DH2 (inactive)"
 /*tag= n
/note= "ACP6"
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/note= "ACp4"
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/note= "ACP3"
                                      /*tag= o
/not.e= "KR6"
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/note= "ER6"
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/not.e= "KS6"
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/note= "KR5"
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/note= "AT5"
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/note= "ACP2"
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/note= "KS5"
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/note= "AT4"
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/note- "KS4"
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/note= "KR3"
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/note= "AT3"
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/note= "KR2"
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FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; Streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveitis; alopecia universalis; autoimmune chronic active hepatitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; neutite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss.
                                                                                                                                                                                                                Nucleotide sequence of the FK-520 biosynthetic gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "fkb1 gene"
complement (10987..11247)
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/note= "fkbc gene"
complement (13452..13662)
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complement (12113..13150)
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complement (13212..23988)
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complement (9894..10994)
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/note= "fkbw gene"
complement (2020.3579)
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complement (4595..5488)
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complement (412..1836)
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= "fkbRl gene"
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/note= "fkbv gene"
3969..4496
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* "fkbE gene"
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note= "fkbG qene"
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                                                                                                                                         AAA14651 standard; DNA; 77536 BP
                                                                    1368 agacgacgacgacaaacccga 1388
                                                                                                                                                                                                                                                                                                                                                              Streptomyces hygroscopicus.
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/*tag=_ _
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61220 cgaccccgaggacatacccacccgcgcccacccgcgccacccgcgtcctgaccgcct 61279
                                                                               61400 cctcatcgaaaccgaccccracacccccccccctggcccaaccgccaccccccgg 61459
                                                                                                                                                                                                                                                 61580 cggctccggcaccttcgccggcatcctcgccgccacctgaaccaccccacct 61639
                                                                                                                                                                                                                                                                                          61640 ecteleccygeaceccaceccecqacyccacecccggcaceccectgcgacqlegg 61699
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                                                                                                            1008 glaccccogycgatettcgaecacggcacaccctggcgctgtatcacaccaaacgcet 1067
                                                                                                                                                    1068 agcolococqqcccaqcqqalcalqclqllcqccaacgaccgcggctgcaccaaaccgy 1127
                                                                                                                                                                                            1248 aggetggancacceaeaacacceaeggecacaceqaatggetaceaeceaeceaece 1307
                                                                                                                                                                                                                                                                                                                        cgaccacggcraacrrgcaccaacaccttccaccaccacgaatcctccacaacca 1367
                           888 cctgaccgacctgcaaaccggcgccggcaagggcttcaccggcggcggcaccctgctacr 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis; multifunctional enzyme; polyketide; avermectin; veterinary drug; agrochemical; ds.
                                                                                                                                                                 S. avermitilis avermectin aylycon synthase DNA aveAII SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..14646
/*tag* a
/*tag* a
14824..31422
/*tag* b
/*tag* b
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA92302 standard; DNA; 31422 BP
                                                                                                                                                                                                                                                                                                                                                                1368 agacgacgardarauaccega 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0046961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avermitilis.
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6.3%; Score 87.4; DB 21; Length 77536;
Best Local Similarity 47.2%; Pred. No. 1e-07;
Matches 265; Conservative 0; Mismatches 296; Indels 0;
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complement (43144..43660)
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complement (43777..44629)
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16754..47788
  complement (35749..37144)
                                                              somplement (38371..38581)
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                              complement (37145..38296)
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                                                                                            complement (38677..39307)
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/note= *AT8"
60399.61412
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/note= "DH8 (inactive)"
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/note=_ fkbp gene"
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/note=-#fkbo gene"
17785..52272
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/*tag= bc
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/*tag= bd
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57990..59243
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The present sequence represents DNA which encodes avermectin aglycon synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA; (2) expression vectors containing the DNA; (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformants; (5) preparation of avermectin aglycon or its derivatives by culture of transformed overmectin-producing microorganisms; and (6) oligonucleotides of 5-60 bases in length containing sense or antisense sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified forms of avermectin and of the intermediates in its blosynthesis, for use as drugs, veterinary drugs and agrochemicals.
                                                                                                                    Avermectin aglycone synthase DNA and proteins encoded by all or part it for the production of avermectin and its derivatives for drug and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;
                                                                                                                                                                                                               Claim 2; Page 134-203; 314pp; Japanese
                                                                      P-PSDB; AAB23751, AAB23752.
                                                WPI; 2000-565458/52
  Ikeda H;
                                                                                                                                                                    agrochemical use
  Omura S,
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21; Length 31422; Indels Score 86.6; DB 21; Pred. No. 1.4e-07; 0; Mismatches 489; 6.2%; Best Local Similarity 40.7 Matches 451; Conservative Query Match

22152 cacccacccgtcttcgocg&cgcactcaacgacatctgcaccacctcgaccccacct 22211 egaccaccectectecectecteacecaggaceceaacacecaggacacecacect 22271 743 504 gctggcccgctacgcccagcgggtcatggactggctacaccccgacggcgacctcaccga 563 caccegccaggccgccgaagccgacctggccggcaaagccgctcaatatcgtcccgacga 503 22332 ccaygicgccetccace--gcctcctcaccgacggctaccacatcaccrrccartar caccgaacgcgccacaacgcggcatcacctgagcaaccagcaatacgacggcatgtc acggctaagtggctacctgacccccaagcgcgggccacctttgaagccgtgctagcraa 444 624 564 22272 22212 ò ŏ d qq Op ð à ò

684 actggccgccccgggggggaccacccgacgacacacacccggtcatcuacucvacvor geoggacacteceteggega-aateacegeegeececetegeeggeatecteaecoloac 744 22390 g Ω QQ

854 22509 catgaccacctccacaccacccccaccacatcacccacatcaccgcccacgaaaa 855 cggtcttcccgtctcgatcgtggtcaccaccac----cctgaccgacctgcaaaccgg gctggccgggctgcgcg-----ctgatcgcctccgggaaactgggccaacaca 804 Qγ g ò

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22689 caccaaccacgccttccactccccacaacccaactccaccagra gaccagccacgccactactccccgcaagcgggaggtaccccaggcgatcttcga 696

ccaeggeacacecetggegetgtateacaceaaegeetageeteeeeggeeeagey

1029 22749

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catgotyltogccaacgaccgcggctgcaccaaacccggctgtgacgcaccggcctacca 1148 1206 getgaccrtggcctgggcccqqqqaqaqcgartcgccqaaaaaggctggaccacccaca 22929 caacaccctcaccarcctcacccacacccccaccaccaccaccacccctcac caccaacactteraccaccegaangaltectecacaaccaagacgacgacaaace 1149 cagrecaagrecarrurgleacegrelygaecageaceggacaterrunenga 22869 caccaccarreaurecircarradus y popular actacatega actega arrega caacacccacggcracaccgaatggctaccacccracctcgaccacggccaacccc c 23109 c 1386 1266 1326 1386 23109 g qq q ŏ ò ŏ g ò

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Sequence

Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 4,

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1789587 GCATCACCAAGCCCGACGCCGCCCGCCCACGCCGACGCCGCCGATCTCGGACCTCGTC 1789528
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Pred. No. 1e-266;
0; Mismatches 21; Indels
US-07-951-715A-2
US-08-459-54BA-2
US-08-459-55A-2
US-08-459-504B-2
US-08-459-444-2
US-09-053-549-3
US-09-474-933-1
US-09-474-933-1
US-09-474-933-1
US-08-387-942C-1
US-08-387-942C-1
US-08-387-942C-1
US-08-459-44BA-3
US-08-459-444B-3
US-08-459-504B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQUENCE 1. APPLICATION 05/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: FRASER, COMEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SCOTRANKE: PATENTIN VENTER: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEC ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL. I GNMENTS
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1789527 GAGCACTCACCGGTGAACCGCTAGCCCCACAGTTGACCGCCACCGCCCACCGCCCAACGCC 1789468
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RESULT 2 US-08-390-878-18

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67 tggacgaggtgtcltttgaggtgttgaccaccccagaacggctgcggtctctggaacgtc 126
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Sequence 18, Application US/08390878
Patent No. 5700683
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                   ... lownsend and Townsend Khourie and Crew
One Market Plaza, Steuart Street Tower, 20th
Floor
                                                                                                                                                                                                                                                                                                                                      Version #1.30
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Pred. No. 3.3e-246;
0; Mismatches 51;
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HULLEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic) US-08-390-878-18
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
                                                                                                           18
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                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                              ZIP: 94105
                                                                                                                                            ADDRESSEE:
STREET: Or
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acaccccgacggcgacctcaccgacaccgaacgcgcccgcaaacgcggcatcaccctgag
                                                              Sequence 1, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses
                                                                                                                                                                    gatecgeatgaceageceacgeceactacteceeegeaageggaaggtaceeeagge
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US-08-464-052-1
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                                                                                                                                                     OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%; Score 455; DB 3; 1
100.0%; Pred. No. 3.9e-88;
ive 0; Mismatches 0;
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CLASSIFICATION:
ATTORNEY FAGENT INTERMATION.
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (715) 263-1304
TELEPHONE: (715) 263-1304
TELEPHONE: (715) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
TELEPHONE: (716) 263-1600
TENGTH: 1535 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                           E: Nixon, Hargrave, Devans & Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acgacgggctgctggccgggctgcgctgatc
                                                                                                                                                                                                     APPLICATION NUMBER: US/08/464,052 FILING DATE:
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
            CORRESPONDENCE ADDRESS:
                                                                                                                COMPUTER READABLE FORM:
SEQUENCES:
                                                                      New York
(: U.S.A.
                                        STREET: Clinton
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 455; Conserv
                                                                                                    14603
                             ADDRESSEE:
                                                                                   COUNTRY:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION 194Ps: US/08/689,411
                                                                                                                                                                                                                                                                               ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
TTY: Rochester STATE: New York
        19603/187
                                                                                                      Sequence 1, Application US/08689411
Fatent No. 6224881
GENERAL INFORMATION.
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pole
TITLE OF INVENTION: CELLULAR UPTAITIE OF INVENTION: TEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/JOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.05
Matches 455; Conservative
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 14603
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                                                                        RESULT 5
US-08-689-411-1
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                                              APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
CORRESPONDENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Michael L.

REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (716) 263-1304

TELEFAX: (716) 263-1304

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1535 base pairs*
                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.7%; Score 455; DB 4; 100.0%; Pred. No. 3.9e-88; iive 0; Mismatches 0;
                                                                                                                                 ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acgacgggctgctggccgggctgcgcgctgatc 828
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/461,002
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
Sequence 1, Application US/08461002
Patent No. 6214543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.7
Best Local Similarity 100.
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                                   ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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DNA MOLECULE FRAGMENTS ENCODING FOR
CELLULAR UPFAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
THERROF
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100.0%; Pred. No. 3.9e-88;
o. Mismatches 0; Indels
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1127 TGCTAGCCAAACTGGCCGCCCCGGGGCGACCAACCCCGACACACCCCGGTCATCG 1186
                                                            734 acaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaacc 793
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                                                                                                                                                                                                            Sequence 1, Application PC/TUS9409863
GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR
TITLE OF INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
FELECOMMUNICATION INFORMATION:
TELEPHONE: (716,263-1600
TELEFAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE :HARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                    ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09863
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PCT-US94-09863-1
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                     New York
U.S.A.
                                                                                                                                                                                                 PCT-US94-09863-1
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STATE: NE
COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                 614 acggcatglcacggctaagtggctacctgacccccaagcgcgggccacctttgaagccg 673
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Computible OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6008201
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 5:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 650 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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APPLICANT: Kiley M.D., Lee W.
APPLICANT: Chong, Pole
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
    673 gigetagecaaaciyyeegeeeeygegaeeaaeeregaegaegaegaeeayiteale 732
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APPLICATION NUMBER: US/UN/AB9.411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                100.0%; Pred. ...
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C'ERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Parts
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; Patent No. 6224881
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TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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(716) 263-1600
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nucleic acid
EDNESS: double
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Best Local Similarity 100°
Matches 396; Conservative
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CITY: Rochester
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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121 GACCTCACCGACACCGAACGCCCCGCAAACGCGGCATCACCTGAGCAACCAGCAATAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERBENCE/OCKET NUMBER: 19603/186 (D-1485B)
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
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Pred. No. 1e-75;
                                                                                                                                                                                             ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
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100.0%; Pred. No. 10.00.00; Mismatches
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Patent No. 6214543
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US-08-461-002-5
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nucleic acid
DNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: New York
COUNTRY: U.S.A.
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; OTHER INFORMATION: "n" bases at various positions throughout the
;; OTHER INFORMATION: represent a, t, c or g
0S-09-103-840A-2
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Pred. No. 1.3e-12;
0; Mismatches 20;
                                                                                                                                                                                                                              APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENERR, Claire M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
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Best Local Similarity 98.5%;
Matches 1327; Conservative (
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                                   ctcgtcgagcactcaccggtgaaccgctagccccacagttgaccgccaccgccaccgccc
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      Db 3883702 ttgacgcccaagccagcgaggaagaactgggcggcggcgctgtyctgcgcgctgtycraarc
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                                                                                                                                                        FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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                                                                                                                                                                                                                                                                                                                                                  7.3%; Score 101.2; DB 4;
100.0%; Pred. No. 1.3e-12;
11ve 0; Mismatches 0;
                                                                                                             APPLICANT: WHITE, Owen K.
APPLICANT: WHITE, Owen K.
APPLICANT: WENGER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
  ccgtggacctgtgagatacactacacc 3870762
                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                             Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                       Ö.
                                                                                                       Robert
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 1393; Conservative
                                                                                       GENERAL INFORMATION:
APPLICANT: FLEISCHMAN,
                                                                                                                                                                                                                                                           LENGTH: 4411529
                                   RESULT 11
US-09-103-840A-1
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Db 3870736
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3884242 accccggtcatcgacaccacccgatgcgccgcatcgacaccgcagccaa 3884301
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Db 3884422 caaaccggcgccggcaagggctLcarcggcggcggcaccctgctacccatggccgatgtg 3884481
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DNA SEQUENCES.
TITLE OF INVENTION: DNA SEQUENCES.
TITLE OF INVENTION: DNA SEQUENCES.
TITLE OF INVENTION: 1996-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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661 acctttgaagccgtgctagccaaactygccgccccggcgcgaccaacccgacgaccac
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Db 1780705 CGAATAGCCGGAGGAGTTGTCGAGGTCTTTGATGCGCTGGATGCCGAGCTGGACCGCT 1780646
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                                                                                      Length 4403765,
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                                                                                    Score 78.4; DB 4;
Pred. No. 8.9e-08;
0; Mismatches 39;
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t, c or
TYPE: DNA
CRGANISM: Mycobacterium tuberculosis
FEATURE:
O'THER INFORMATION: CDC 1551
O'THER INFORMATION: "n" bases at varic
O'THER INFORMATION: represent a, t, c
US-09-103-840A-2
                                                                                    Similarity 97.2%;
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Db 1779625 ATCATGCTGTTCGCCAACGACGCGCGCTGCAAACCCGGCTGTGACGCGGCCTAC 1779566
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Best Local Similarity 43.1
Matches 342; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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CURRENT APPLICATION DATA:

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APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Makavas, Stephan J.
APPLICANT: Navas, Stephan J.
APPLICANT: ARAVAS, Stephan J.
APPLICANT: ARAVAS, STEPHAN J.
APPLICANT: MAKAVAS, STEPHAN J.
APPLICANT: ARAVAS, STEPHAN J.
ARAVAS, ARAVAS, STEPHAN J.
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ARAVAS, ARAVAS, STEPHAN J.
ARAVAS, ARAV
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Patent No. 6060234
GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version
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Pred. No. 1.2e-06;
D; Mismatches 275; Indels
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                                                                                                                               NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEFAX: (847)-938-3137
TELEFAX: (847)-938-2623
MBER: US/08/858,003
16-MAY-1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           788 TCCCCACCACCGCCGCAACCAACGAAG
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Sequence 1, Application US/09078166

Patent No. 6063561

GENERAL INFORMATION:

APPLICANT: Ratz, Leonard

APPLICANT: Stassi, Diane L.

APPLICANT: Summers Jr., Richard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
 APPLICATION NUMBER: US/08/
FILING DATE: 16 MAY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORREY/AGENT INFORMATION:
NAME: Dianne Casulo
                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%;
                                                                                                                                                                                                                                                                                                  : 925 base pairs
nucleic acid
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 235; Conservative
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US-08-858-003-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic
STRANDEDNESS:
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APPLICANT: Ruan, Xiaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.0%; Score 70; DB 3; Length 925 Best Local Similarity 46.1%; Pred. No. 1.2e-06; Matches 235; Conservative 0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOCTHALE: FRASLEG VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,166
FILING DATE: 16-MAY-1979
CLASSIFICATION:
PROOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERNICE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
                                                                                                                                      ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: 111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Search completed: April 3, 2002, 05:46:33 Job time: 33753 sec

Perfect score: Scoring table:

Sequence:

Minimum DB : Maximum DB :

Database

Searched:

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OM nucleic

Run on:

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AQ748706 HS_5540_A

BG809582 mgct001xa

AL572700 AL572700

BF234665 HVSMEf001

BF24665 HVSMEf001

BF256679 HVCEG001

BF26679 HVCEG001

BF267681 HVCEG001

BF267681 HVCEG001

BF256781 HVCEG001

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BF25675 HVSMEf001

BF266876 HVSMEf001

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BF266876 HVSMEf001

BF266876 HVSMEf001

BF2668876 HVSMEf001

BF2668876 HVSMEf001

BF266888 HVSMEf001

BF26688 MGCL001xc

BF369968 MGCL001xc

BF369968 MGCL001xc
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/clone="hasp001xa01f"
/clone_lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Heterobasidion annosum/Finus sylvestris mixed EST library. Heterobasidion annosum/Finus sylvestris mixed EST library Eukaryota: mixed EST libraries.

1 (bases 1 to 197)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with Monthlished (2001)
                                                                                                                                                                                                                                                                                                                                                                       haspoolxaolf Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Heterobasidion annosum/Pinus sylvestris mixed EST library CDNA clone hasp001xa01f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Heterobasidion annosum/Pinus sylvestris
EST library"
                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred Asiegbu@mykopat.slu.se
Seg primer: T7 primer
Location/Qualifiers
1. 1197
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           AQ748706
BG809582
AL572700
BE034822
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AQ782679
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BE421615
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DEFINITION
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TITLE
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COMMENT
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B1416575 hasp001xe
BF260036 HVSME6002
A186419 w152f10.x
B1416699 hasp001xp
BF628951 HVSMEb000
AL249930 Tetraodon
BG786255 SEAUWC006
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                                                     2, 2002, 18:47:35 ; Search time 3835.7 Seconds
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  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                     11351937 seqs, 5372889281 residues
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                                    nucleic search, using sw model
                                                                                                                                                                                                                                        summaries
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B1416650
B1416530
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B1416575
BF260036
A1864419
BF62695
BF62695
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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hasp001xm GA\_Eb004 SP\_1038\_B

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105.2 104.6 100.4 99.2 98.4 98.9 97.2 96.6 95.8 95.8

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/dev_stage="Seedling roots of scots pine were infected 6 days with H. annosum."

//note="Vector: pT-Adv: Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)."

// 185 others
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                                                                                                       DB 11; Length 1197;
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Pred. No. 3.2e-09;
0; Mismatches 666;
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/clone | briteterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp)"
/dev_stage-"Seedling roots of scots pine were infected for days with H. annosum.
/note="Vector: pT-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750
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Tel: +46 18 67 15 90
Fax: +46 18 30 92 45
Email: Fred.Asiegbuenykopat.slu.se
Seq primer: T7 primer.
Seq primer: T7 primer.
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
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Eukaryota; mixed EST libraries.
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                                                                                                                                                                                                                                                                                                                                     Tel: 46 18 67 15 98
Fax: 46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: Y7 primer.
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/clone="hasp001xm01f"
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVSMEh0096624f Hordeum vulgare 5-45 DAP spike EST library HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0096G24f, BE455162
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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                                                                                                                                         942 gctacccatggccgatgtgatccgcatgaccagccacgccaccactactccccgcaag 1001
                                                                                                                                                                                                    cgggaggtacccccaggcgatcttcgaccacggcacaccctggcgctgtatcacaccaa 1061
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                                                                                                         cgaaaaaggetggaccaccacaacaacacccacggccacacgaatggctaccaccacc 1301
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                                                      882 caccacctgaccgacctgcaaaccggcgccggcaagggcttcaccggcggcggcacct
                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
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Unpublished (2000)
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Fax: 864 656 4293
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/organism="Hordeum vulgare"
/cultivar="Morex"
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/dultivar="Morex"
/dultivar="Morex"
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/clone="HYSMEN0096G24f"
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1 (bases 1 to 931)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with
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            tggcctgcggccccgacaaccgactcyccgaaaaaggctggaccaccacaacaacaaca 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="hasp001xe15f"
/clone=lb="heterobasidion annosum - Scots pine infection
/clone_lb="heterobasidion annosum - Scots pine were infected
/dev_stage="Seedling roots of scots pine were infected for
/dev_stage="Seedling roots of scots pine were infected for
/day_with H. annosum"
/note="weetor: pr-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
pine roots infected for 6-days with mycelia of
14 c 1063 g 38 t 59 others
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                                                                                                                                                                                                                                                      Heterobasidion annosum/Pinus sylvestris mixed EST library.
Heterobasidion annosum/Pinus sylvestris mixed EST library.
Heterobasidion annosum/Pinus sylvestris mixed EST library
L Waryotes and EST libraries.
L (bases 1 to 1224)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected CDNA clones from the seedling roots of Scots pine (Pinus sylvestris)
Compublished (2001)
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,

    1. .1224
    /organism="Heterobasidion annosum/Pinus sylvestris mixed
EST library"

                                                                                                     B1416537 1224 bp mRNA EST 15-AUG-2001 haspOUDxel5f Heterobasidion annosum · Scots pine infection stage subtraction cDNA library (hasp) Heterobasidion annosum/Pinus sylvestris mixed EST library cDNA clone haspOUlxel5f, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 gatcggcgaggcgcacgtcaaagtgattcgcgccctttttcgcccacctgcccgccgcg 433
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151 CCCCCCCCCCCCCCCCCCCCCCCCCCCCTTNCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:169015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7 primer,
Location/Qualifiers
                                                                                                                                                                                                                    BI416537.1 GI:15187560
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Best Local 3
                                                        RESULT 5
BI416537/c
LOCUS
DEFINITION
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/clone="hasp@olxg15f"
/clone=lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
/dev_stage="Seedling roots of scots pine were infected for
/days with H. annosum*
/note="Weetor: pp-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycella of
Hetcoasidon annosum (FP5)." 16 others
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EST library"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98; DB 11; Length 93
Pred. No. 5.8e-08;
0; Mismatches 461; Indels
   Scots pine (Pinus sylvestris)
seedling roots of Scots pine (Pinus syl
Unpublished (2001)
Contact: Fred O. Asiegbu
Debt. of Forest Mycology & Pathology
Swedish University of Agriculture, Box
                                                                                                  Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
                                                                                                                                                                                                                                      /db_xref="taxon:169015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%;
Best Local Similarity 44.2%;
Matches 365; Conservative
                                                                                         Sweden
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/note="Vector: lambdaZAP, Site_1: EcoR1; Site_2: Xhol: For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To see http://www.genome.clemson.edu/orders" a clone see http://www.genome.clemson.edu/orders" 819 c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                           BF260036 1159 bp mRNA EST 23-FEB-2001
HVSMEf0020024f Hordeum vulgare seedling root EST library HVcDNA0007
(etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEf0020024f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Triticeae; Hordeum.
1 (bases 1 Lo 1159)
Wing R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development of a genetically and physically anchored EST resource
                                                                                                                        cacaacaacaccaacgeccacaccgaatggclaccaccacccacctcgaccacggccaa 1320
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HVCDNA0007 (etiolated and unstressed)"
/tissue_Lype="Seedling root"
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                                                                                                                                                                                               Score 97.2; DB 11;
Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Hordeum vulgare"
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High quality sequence stop: 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
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Unpublished (2000)
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Best Local 9
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                                                                                                                               1261
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AUTHORS
                                                                                                                                                                                                     1321
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KEYWORDS
SOURCE
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BF260036
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/I.LNL at:

Mow-bio. Inh.gov/bhrp/jmaqe.html

Insert Length: 621 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 282.

Location/Qualifiers
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National Cancer Institute / National Institute of Neurold
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                    M.D., Myrna
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Pred. No. 9.3e-08;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI416699
BI416699.1 GI:15187722
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stage subtraction cDNA library (hasp)"

for stage="Seadling roots of scots pine were infected for 6 days with H. annosum"

/note="Weetor: pT-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots heterobasident for 6-days with mycelia of Heterobasident property of the property of th
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/clone_lib="Heterobasidion annosum - Scots pine infection
                            Heterobasidion annosum/Plnus sylvestris mixed EST library. Eukaryota; mixed EST library Eukaryota; mixed EST library Eukaryota; mixed EST library Eukaryota; mixed EST library 1 (bases 1 to 863)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A. for andomy selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Conteact: Fred O. Aslegbu
Conteact: Fred O. Aslegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eggeegeeategacegegacaceegeageeaageecaacgeaaceaegaegggetgetgg 808
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Pred. No. 1.4e-07;
0; Mismatches 386; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 446 18 67 15 98
Fax: 446 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1. (bases 1 to 1348)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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253 ccaagcccgacgcccggccggcatcgccgacgccgatctcggacctcgtcgagcan; 312
                                                                                                                                                                                                                                                                                                                                                          HVSMEb0009E241 Hordenm vulgare seedling shoot EST library HVCDMEb0009E245 inRNA sequence. HVCDMEb0009E23f, mRNA sequence.
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Clemson University Genomics Institute
Clemson University
To Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="TJC121"
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Seg primer: AATMACCCTAAAGGG
High quality sequence start: 6
High quality sequence stop: 1310.
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clonne-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.qenoscope.ons.fr/Tetraodon.
Location/Qualifiers
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library G from Tetraodon nigroviridis, genomic survey
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Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodoutiformes;
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1 (bases 1 to 1016)
1 Roses-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Tetraodon nigroviridis DNA sequence
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cost.crollius.H., Jaillon,O., Dasilva,C., Bouneau,L., Fish
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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/db_xref-"taxon:99883"
/clone="036F09"
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Harity 45.2%; Pred. No. 1.6c-07;
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630 aagtggctacctgacccccaagcggggccacctttgaagccgtgctagccaaactggc 689	750 ggccgccatcgacgcgacaccgcagccaacgccaacgcaacgcaacgacg	CGGCCCGCCCGCCCGCCCGCCCGCCGCCGCCGCCCGCC	430 CGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	990 ctccccgcaagcgggaggtaccccaggcgatcttcgaccacggcacaccctggcgct 1049 	0 gtatcacaccaaacgcctagcctccccggcccagcggtcatgctgttcgccaacgaccg 1109 			30 caaccgactcgccgaaaaggctggaccaccacaacaacaccacggccac 128  	12  BG786255 825 bp mRNA EST 20 MAY-2001 SEAUROOGO212 Sea urchin primary mesenchyme cell chNA ibblary Strongylocentrotus purpuratus chNA clone PC_0028_A2_A0U8 MK 5', mkNA sequence.  N BG786255 GI:14157268 BG786255 I GI:14157268 BG786255.1 GI:1416767 BG7862567 BG7867 BG7862567 BG7867
Oy 63 Db 69 Oy 69	Oy 75 Db 57 Oy 81	0b 51		Qy 990 Db 331	Qy 1050 Db 271	Qy 1110 Db 211	Qy 1170 Db 153	Qy 1230 Db 93	RESULT 12 BG786255/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

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/tissuc_type-"cmbryo"
/ccll_Lype="primary mesenchyme cells"
/ccll_Lype="F.col"
/lab_host-"F.col"
/locle-"Vector: psiOkT1; Site_1: NotI: Site_2: Sall; oligo
dt priming from poly A+ RNA, directionally cloned"

0 c 667 g 117 t 34 others
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/organism="Strongylocentrotus purpuratus"
/db_xxef="taxon:7668"
/clone="Pc_0028_A2_A08_MR"
/clone="tpc_01b="Sea urchin primary mesenchyme cell cDNA library"
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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            AQ895329 918 bp DNA GSS 10-NOV-1999 HS_4832_A2_HOl_T7A CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4832 Col=2 Row=0, DNA sequence.
                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                      Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 95; DB 13; Length 918; 46.6%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 others
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/clone="Plate=4832 Col=2 Row=0"
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1 (bases 1 to 966)
Mahairas,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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University of Washington
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: javallace@u.washington.edu
Clones are derived from the human BAC library RPCI-II. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.butfalo.edu). Clones may be purchased from
BACPAC Resources (http://wargac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genelics (info@resgen.com). BAC end Web Server:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1004 ggaggtacccccaggcgatcttcgaccacggcacacccctggcgctgtatcacaccaaac 1063
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                                  .064 gectagectecegggeceageggateatgetgttegeeaaegaeeggggetgeaceaaae
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99780'stry
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/db_xref="taxon:9606"
/clone="plate=1116 Col=6 Row=A"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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                                                                            Score 95; DB 13;
Pred. No. 2e-07;
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Matches 293; Conservative
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/note="vector: pBlueScript SK(+) Vector; Site_1: EcoRI; Site_2: Xho1; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."
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                                                                                                                                                        Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Fax: 919-513-0024
Email: ralph_dean@ucsu.edn
Seq primer: T3 primer (AATTTAACCCTCACTAAAGGG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 94.4; DB 11;
45.4%; Pred. No. 2.5e-07;
Live 0; Mismatches 381;
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surface"
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                                                                       Construction and sequence
library in the rice blast
Unpublished (2001)
Contact: Ralph A. Dean
  Sordariomycetes incert
1 (bases 1 to 782)
Choi, W. and Dean, R.A.
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Best Local Similarity 45.4
Matches 317; Conservative
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Search completed: April 2, 2002, 21:47:49 Job time: 10814 sec

us-09-785-904-2.rng

		cDNA encoding huma cardiotrophi Human cardiotrophi cDNA encoding nove Human PROBB2 cDNA.  M. tuberculosis im Mycobacterium tube M. tuberculosis an M. tuberculosis an M. tuberculosis re cuberculosis an collection of the collectio	
47.8 10.6 2697 13 47.2 10.4 1000 21 47.2 10.4 1454 20 45.6 10.3 1337 20 45.6 10.1 114955 20 45.6 10.1 4478 21 45.6 10.1 4547 21 45.6 10.1 4547 21	20 45.6 10.1 4571 21 AAA14662 21 45.6 10.1 7536 21 AAA14665 22 45.4 10.0 2888 17 AAA12651 24 45.4 10.0 2888 17 AAA29568 25 43.4 9.6 6085 18 AAA70153 26 43.4 9.6 1028 22 AAA70153 27 43.4 9.6 1028 22 AAA91542 28 43.2 9.5 1107 22 AAA14540 29 43.2 9.5 2712 20 AAA0825 31 42.6 9.4 1018 16 AAT02326 23 42.6 9.4 1203 20 AAZ00869 2 34 42.6 9.4 1485 21 AAZ00869 2 43.6 9.4 1485 21 AAZ00869	37  42.6 9.4 1539 21 38 42.6 9.4 1539 21 39 42.6 9.4 1539 21 40 42.6 9.4 1539 21 42 42.6 9.4 1539 22 42 42.4 9.4 494 199 44 42.4 9.4 494 199 44 49.4 9.4 494 199 45 42.4 9.4 494 20 45 42.4 9.4 494 19 42.4 9.4 40.4 9.4 494 19 42.4 9.4 49.4 9.4 49.4 9.4 49.4 9.4 49.4 9.4	XX XX XX XX XX Yycobacterium tuberculosis. FT CDS 1.1535 XX XY XX
GenCore version 4.5  Copyright (c) 1993 - 2000 Compugen Ltd.  nucleic search, using sw model  April 2, 2002, 22:47:50; Search time 366.19 Seconds (without alignments)	US-09-785-904-2  US-09-785-904-2  1 gatcggcgacgacatcaccgggctgcgcgcgqttq 453  1 lest IDENTITY_NUC Gapop 10.0 , Gapext 1.0  930621 seqs, 428662619 residues  1 of hits satisfying chosen parameters: 1861242  seq length: 0  seq length: 2000000000	### ALTAINUM MATCH 100* Listing first 45 summaries Listing first 45 summaries    SIDS2/gcgdata/geneseq/geneseqn/NA1981 DAT:*   SIDS2/gcgdata/geneseqn/NA1981 DAT:*   SIDS2/gcgdata/geneseqn/NA1981 DAT:*   SIDS2/gcgdata/geneseqn/NA1983 DAT:*   SIDS2/gcgdata/geneseqn/NA1984 DAT:*   SIDS2/gcgdata/geneseqn/NA1985 DAT:*   SIDS2/gcgdata/geneseqn/NA1985 DAT:*   SIDS2/gcgdata/geneseqn/NA1989 DAT:*   SIDS2/gcgdata/geneseqn/NA1989 DAT:*   SIDS2/gcgdata/geneseqn/NA1989 DAT:*   SIDS2/gcgdata/geneseqn/NA1989 DAT:*   SIDS2/gcgdata/geneseqn/NA1999 DAT:*   SIDS2/gcgdata/geneseqn/NA199 DAT:*	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.   SUMMARIES

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                                                                                                                                                                                                             Gaps
                                                           The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAK71931.
                                                                                                                                                                                                                                1 gatcggcgaggcgcacatcaaagtgattcgcgcctttttcgcccacctgccgcgcg
                                                                                                                                                                                                                                           4;
                                                                                                                                                                                        DB 16; Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell entry; macrophage; passive immunisation;
DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
                                                                                                                                                                                        90.2%; Score 408.4; DB 16; Length
97.8%; Pred. No. 1.1e-78;
tive 0; Mismatches 6; Indels
                                                                                                                                                          Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis cellular uptake gene region.
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181..810
                                             Claim 2; Page 9-11; 46pp; English.
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Best Local Similarity 97.8
Matches 446; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 gtgctagccaaactggccgcccggggcgaccaacccgacgaccacaccccggtcalc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 accteaccyacaccyaacycgeregeaacge-geateaccetgageaaccageaatacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 408.4; DB 17; Length 1545;
Pred. No. 1.1e-78;
); Mismatches 6; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                          /product= macrophage survival protein
                  entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  materials, e.q. therapeutic genes.
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              /product= cell e
886.1535
/*tag= b
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/label- ORF-2
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Best Local Similarity 97.8%;
Matches 446; Conservative (
/label= ORF-1
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1406..10673
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                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis strain BCG
                                                                                                                                                                                                                                                                                                                    AAT33537 standard; DNA; 12412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtcccgacgagctggcccgctacgcccagogggtcatggactggctacaccccgacqgcg 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enhance uptake of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within mariophayes. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DMA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tggatgtgtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 408.4; DB 19; Length 1535;
Pred. No. 1.1e-78;
); Mismatches 6; Indels 4;
                                                                                                                                                                                  DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis DNA - confers ability therapeutic agents e.g. antibiotics, also useful
                                                                                                                                                                                                          Cellular uptake protein; vaccine; infection; ds.
                                 /note= "stop codon not given"
                     cacgacgggctgctggccgggctgcgcgctgatc 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Pages 9-10; 82pp; English.
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/*tag= a
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ilarity 97.8%;
Conservative (
                                                                                                            AAV18647 standard; DNA; 1535
                                                                                                                                                                                                                                                                                                                                                                                                 96US-0689411.
                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-145620/13.
P-PSDB; MW47541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riley LW;
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                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1996;
                                                                                                                                                                                                                                                                                                                            W09805784-A1
                                                                                                                                                            03-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chong P,
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1067 acggeatyleacgyetaagtggelacetgaecececaag-egegggecacetttyaagee 1125
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                                                                                                                                                                                                                                                               gigotagecaaactggeegeeeeeeggegegaceaaceeegaceacaceeeggicaic 357
                                                                                                                                     acggcatglcacggctaaglggctacctgacccccaagtcgcggggcacctttgaagcc
                                                                                                                                                                                                                                                                                                         gacaccarrecental yeggeegneating togaecaccaccaccaccaageccaageccaacyeaae
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/wote= "BCG delta l deletion region"
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                                                                                                                                      aggegeacateaaagtgattegegeeetttttegeee--acetgeeegeggggggggtg 66
the deletion; the deletions are detected either by detecting the presence or absense of deletion junctions (see AAT3358-46), or by detectin the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                             caccgacaccgaacgcgcccgcaaacgc-gcatcaccctgagcaaccagcaatacgacyg
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                                                                                               Length 12412;
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                                                              Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
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                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis strain H37Ra (ATCC 25177)
                                                                                             Score 366.8; DB 17;
Pred. No. 9.1e-70;
0; Mismatches 12; I
                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis macrophage survival gene.
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95.6%;
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                                                                                                                  Conservative
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Best Local Similarity
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A DNA molecule (AAT33658) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT33656) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript I vector and screening recombinant E. coli strains for Hela cellinvasive clones. It can be incorporated into a vector and used for prodn of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule tuberculosis the ability to enter mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 egtecegacgaqetqqeecqetacqeecagcqqqtcatggactqqetacaceceqacqgc 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 cgtcccgacgagottggcccgctacgcccagcgggtcatggactggctacaccccgacggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416
                                                                                                                                                                                                                                                                                                                                                                                                                    gtggatgtgtccacccgccaggccgccgaagccgacctgccggcaaaggc--ctcaatat 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                              vaccines to protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgtgctaqccaaactggccgcccqgcgcgaccaaccccgacgaccacacccggtcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 egtyctayccaaactggceyerreeygegegaceaacceegacgaceacaceeegyteat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 egamacmommatgregoroproprogregogamaceegeageceaagecaangeaa
                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                         77.5%; Score 351; DB 17; Length 650; larity 97.7%; Pred. No. 1.9e-66; Conservative 0; Mismatches 5; Indels
                                        DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to p mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                             Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 ccaedacqqqclqctqqccqqqclqcqcqccgate 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular uptake protein; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                     Claim 7; Page 45; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
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WPI; 1996-425086/42.
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Matches 388; Conserv
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                 P-PSDB; AAW02303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                            Query Match
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/note- "avermectin aglycon synthase protein" 11971..30690 /note= "avermectin aglycon synthase protein"

2000WO-JP01041.

Ikeda H;

Location/Qualifiers 1..11919

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/\*tag=

/\*tag= b

(first entry)

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Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis; multifunctional enzyme; polyketide; avermectin; veterinary drug;
                                                               S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-565458/52.
P-PSDB; AAB23749, AAB23750.
                                                                                                                                         Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                    (KITA ) KITASATO INST
                                                                                                                 agrochemical; ds.
                                                                                                                                                                                                                                                                  WO200050605-A1
                                                                                                                                                                                                                                                                                                                   23-FEH-2000;
                                                                                                                                                                                                                                                                                                                                          24-FEB-1999;
                                       10-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 egtecegaegagetggeeegetaegeecagegggteatggaetggetaeaeeeeegaeyge 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gaeggeatgteaeggetaagtggetacetgaeeeceeaag-egegggeeaeetttgaage 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 gtggatgtgtccacccgccaggccgccgaagccgacctgccygcaaaggc--ctcaatat 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gtggatgtgtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatat 60
                                                                                                                                                                                                                                      Mycobacterium tuberculosis DNA ^{\circ} confers ability to enhance uptake therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                                                                                                                   The present sequence encodes a Mycobacterium tuberculosis cullular uptake protein fragment, which confers on M. tuberculosis an ability to survive within mercophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in calls of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to me tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtcccgacgagctggcccgctacgcccagcyggtcatggactggctacaccccgacygc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgtgctagccaaactggccgccccggcgcgaccaaccccgacgaccacaccccggtcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 egigetagecaaaciggeegeeeceggegegegaecaacceegaegaecacaeceeggicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgacaccaccccgatgcggccgccatcgaccgcgacaccccgcagccaaqccaacgcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.5%; Score 351; DB 19; 97.7%; Pred. No. 1.9e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 ccacgacgggctgctggccgggctgcgcgctgatc 453
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/*tag= a
/note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                             Disclosure; Page 14; 82pp; English.
                                                                                                                                                  (CORR ) CORNELL RES FOUND INC
                                                                                    97WO-US13056
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                                                                                                                                       (CONN-) CONNAUGHT LAB LTD
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                                                                                                                                                                                                    WPI; 1998-145620/13.
                                                                                                                                                                          Chong P, Riley LW;
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                                                                                                                                                                                                                P-PSDB; AAW47543
                                    W09805784-A1
                                                                                     36-AUG-1997;
                                                                                                              07-AUG-1996;
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synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA: (2) expression vectors containing the DNA: (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformets: (5) preparation of avermectin aglycon or its derivatives by culture of transformets so of the avermectin aglycon microorquisms: and (6) oliqonucleutides of 5-60 bases in length containing sense on antiseuse sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified
Avermectin adjycone synthase DNA and proteins encoded by all or part of it for the production of avermectin and its derivatives for drug and agrochemical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22011 caccaccctcatcacccaacgcgccaccctcatgcaaaccatgccccccggcaccatgac 22070
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use as drugs, veterinary drugs and agrochemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acaccccgacygcyacctcaccgacacygacgcccgcaaacgcgcatcacctgagc 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                     The present sequence represents DNA which encodes avermectin aglycon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 aaccancaatacgacggcatgtcacggctaagtggctacctgacccccaagtcgcgggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 12.6%; Score 57.2; DB 21;
Best Local Similarity 52.5%; Pred. No. 0.00083;
Matches 125; Conservative 0; Mismatches 113;
                                                                                                                                                                            Claim 2; Page 66-134; 314pp; Japanese.
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AAA92301 standard; DNA; 30690 BP

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Best Local S
Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           host cells, and methods for producing novel polyketides by culturing host cells are claimed. The polyketides obtained are useful as antibiotics and insecticides. Fermentation products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with reduction. Novel PKS are provided in which in which the reductive loop in a selected module of the Type I PKS is replaced with the equivalent segment from the same or different PKS gene cluster or by a mutated or synthetic segment. Vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of DNA encoding the first 2 modules of the avermectin polyketide synthase (PKS) of Streptomyces avermitilis. The invention relates to nucleic acids encoding a Type I PKS such as avermectin in which a polylinker with multiple restriction sites replaces or 1 more PKS genes encoding enzymes associated with reduction. Novel PKS are provided in which in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12381 BP; 1884 A; 4561 C; 4005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutated Type I polyketide synthase containing a extension module for replacement of a reductive % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kellenberger JL,
McArthur HAI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing C22-C23 dihydroavermectin, ivermectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7a-f; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             producing polyketides, e.g. Bl avermectin
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                                     285
                                                                                                                                                                                                                                                                               165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis avermectin polyketide synthase modules 1+2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2000
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cacctttgaagccgtgctagccaaactggccgccccggcgcgaccaaccccgacgacca
                                                                                       caccaccctcatcacccaacgcgccaccctcatgcaaaccatgccccccggcaccatgac
                                                                                                                                                  aaccagcaatacgacggcatgtcacggctaagtggctacctgaccccccaagtcgcgggc
                                                                                                                                                                                                           acacteceteggegaaateacegeegeecacetegeeggeateeteaceeteacegaege 9072
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124; Conser
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                              12.3%; 52.1%;
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                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                 Score 55.6; DB 21; Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 1931 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stutzman-Engwall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polylinker site loop sequence, f
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                Length 12381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>B</u>1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vectors and
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                          9132
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                                                                                                                                                                                                                                                                                                                                     0;
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20

165 acacccogacggcgacctcaccgacaccgaacgcgcccgccaaacgcgcatcaccctgagc 224

Matches 124; Query Match Best Local :

Conservative

0;

Pred. No. 0.0018; 0; Mismatches 114; Score 55.6; DB Pred. No. 0.0018

Indels Length

Gaps

0;

DB 21;

31422; 0;

Local Similarity

12.3%; 52.1%;

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RESULT ADAPSOLT ADAPSOLT ADAPSOLT ADAPSOLT ADAPSOLT ADAPS ACCOMENT AND ADAPSOLT ADAP
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                                                                                             or its derivatives by culture of transformed avermectin-producing microorganisms; and (6) oligonucleotides of 5-60 bases in length containing sense or antisense sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified forms of avermectin and of the intermediates in its biosynthesis, for
                                                                                                                                                                                                                                                                 synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA; (2) expression vectors containing the DNA; (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformants; (5) preparation of avermectin aglycon
Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents DNA which encodes avermectin aglycon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 134 203; 314pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agrachemical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avermectin aglycone synthase DNA and proteins encoded by all or part
it for the production of avermectin and its derivatives for drug and
                                                                  use as drugs, veterinary drugs and agrochemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB23751, AAB23752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WP1; 2000-565458/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agrochemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. avermitilis avermectin aglycon synthase DNA aveAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KITA ) KITASATO INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 - AUG - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9193 cyccatcyccyccatcaacacccccacctcctcytcatcaycyycacccccacacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14824..31422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "avermectin aglycon synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .14646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
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RESULT
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Query Match
Best Local Sim
Matches 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                    AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such sequences containing alternatively spliced forms of human IL-Ira. Such sequences are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleac acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-IR). may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1998;
04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IL-1ra BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX02974 standard; DNA; 3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09906426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                       inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of
                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345
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                                                                            Sequence
                                                                                                               inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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                                                                                                                                                                                                                                                                                                                                   Figure 3;
   Conservative
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                                                                               ВP;
                                                                                                             or
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97US-0054646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US16102
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                                                                                                             activity of IL-1 or its receptor
                                                                               807 A;
                  11.6%;
45.6%;
                                                                                                                                                                                                                                                                                                                                    226pp; English
                                                                               847 C;
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   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒP
    Score 52.4; DB 20; Pred. No. 0.008; 0; Mismatches 217;
                                                                                 681 G;
                                                                                 846 T; 17
                                                                                   other;
                                                                                                                  complex.
        Indels
                                    Length
                                       3198;
        0;
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AAA14651/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA14651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3153
                                                                                                                                                                                                                                                                                   autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                  FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; 
Streptomyces hygroscopicus var. ascomyceticus; immunophilm; 
FK-506 bindinų protein; polyketide compound; transplant rejection; 
graft-versus-host disease; uveitis; alopecia universalis;
                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-2000
                                                    CDS
                                                                                   CDS
                                                                                                                                                                                                                                            Streptomyces
                                                                                                                                                                                                                                                               peripheral neuropathy;
                      CDS
                                                                                                                                                                                                                                                                          Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the FK-520 biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209
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                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                           disease; stroke; traumatic spinal cord; brain injury;
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                           hydroscopicus
                                                                                                                                                                                                             complement (412..1836)
                      /note= "fkbF
8156..8824
                                                                                                                  /note= "fkbR2 gene"
complement (4595..5488)
                                                                                                                                                                              complement (2020. 3579)
                                                                                                                                                        /*tag= b
/note= "fkbV gene"
/*tag= g
/note= "fkbG
                                                     6808..8052
                                                             /*tag= e
/note= "fkbE gene"
                                                                                    5601..6818
                                                                                         /*tag= o
/note= "fkbRl gene"
                                                                                                                                                  3969..4496
                                                                                                                                                                                          /note- "fkbW gene"
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Pred. No. 0.04;
0; Mismatches 141;
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RESULT 13
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Best Local Similarity
Matches 154; Conserv
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                                                                                                                                                                                                                 Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor positive breast cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA02484 standard; cDNA; 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim a recombinant enzyme prepn. comprising beta-3-glucanase or a mutant or variant and a vector contg. DNA encodit under the control of an exogenous promoter pref. lac UV5. The example uses the native beta-1, 3-glucanase gene isolated from Oerskovia xanthineolytica genomic DNA and expressed in pUV5-GIS.
                                                                                                                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1469
                                                                                                                                       Homo sapiens
                                                                                                                                                                                          oestrogen receptor-negative breast cancer; lung cancer; ss
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P-PSDB; AAR22197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2697 HP; 402 A; 1004 C; 954 G; 337 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chretien P,
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47.8; DB Pred. No. 0.075; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e enzyme
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    produced by transforming
and free of protease

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1588
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                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAA00010 to AAA02716 represent polynucleotides isolated from cDNA CC libraries constructed from human colon cancer cell lines. The present CC invention also describes a method of detecting differentially expressed CC genes correlated with a cancerous state of a mammalian cell, comprising CC detecting at least one differentially expressed gene product in a test CC sample derived from a cell suspected of being cancerous, where detection CC of the differentially expressed gene product is correlated with a CC cancerous state of the cell from which the test sample was derived. CC The polynucleotides sequences can be used in a method for detecting CC differentially expressed Tenes correlated with a cancerous state of a CC mammalian cell. The polynucleotides can also be used as probes for CC detecting and mapping related genes. They can be used in diagnosis and CC pre-metastatic or metastatic cancerous states, stages of cancer, or cresponsiveness of cancer to therapy). This is particularly for breast cancer, estrogen receptor-positive breast cancer, oestrogen receptor-positive breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams LT, ESCULLE
Reinhard C, Giese K, R
Lamson G, Drmanac R, C
Lamson G, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide library used to determine cancerous states
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
                                                                                                                                                                                                              622
                                                                                                                                                                                                                                                                                                                                   742
                                                                                          502
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   389
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                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                            agccgacctgccggcaaaggcctcaalatcglccrgacgayclggcccgctacurccage 148
                                                                                                                                                                                                                                                                                                                                   cgcgccctttttcgcccacctgcccgccgcqgtggatgtgtccacccgccaggccgaggcoya 88
                                                                                        CCNCCCNNCCCCNGCGNCCTNNCNCCCNNCGNCCCCCNCGCCTCCNCCCCNNCCCCC
                                                                                                                                                     gggtcatggactggctacaccccgacggcgacctcaccgacaccgaacgcgcccgcaaac
                                                                                                                                                                                                                                                                          ccccaagtcgcgggccacctttgaagccgtgctagccaaactggccgcccccggcgca
                                                                                                                                                                              gcgcatcaccctgagcaaccagcaatacgacggcatgtcacggctaagtggctacctgac
gcgacacccgcagccaagcccaacgcaaccacgacgggctgctggccgggctgc 442
                                                          ccaaccccgacgaccaccccggtcatcgacaccaccccgatgcggccgccatcgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer, lung cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 994; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0085426.
98US-0085537.
98US-0085696.
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98US-0105877
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                                                                                                                                                                                                                                                                                                                                                                                                             10.4%;
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Garcia V, Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J, Innis MA,
Randazzo F, I
                                                                                                                                                                                                                                                                                                                                                                                              Score 47.2; DI
Pred. No. 0.09
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                   ປ.097;
ຊື່ 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stache-Crain
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kassam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cf.
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                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                               443
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AAZ17038/c
ID AAZ170
DT DE CONTRACTOR OF CONTRACTOR
                                                                               cc of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The cc polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, anapping, tissue typing or profiling, forensics, genetic analysis and detection of polynuclphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and continued arrays for diagnostics (which may be used to construct a cencoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to condition of genetic predisposition or susceptibility to a disease such as cc andero. The polynucleotides of the invention are especially used in the continues and antagonists can also be used to screen for contride analones and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones WL, Kassam A, Kennedy GC, K
Lamson G, Leshkowitz D, Pot D, Ra
Stache-Crain B, Sudduth-Klinger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic analysis; colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene expression product cDNA sequence SEQ ID NO:4508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ17038 standard; cDNA; 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a library of human polynucleotides comprising the sequences given in AAX12532 to AAX17779. Also described is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human genes and their expression differentially expressed in different c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; gene expression product; diagnosis; therapy; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentially expressed dene product in a test sample from a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2137; 2479pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                              analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980S-0072910.
980S-0075954.
980S-0080114.
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arciu PD, Garcia V, Giese K, Inn
sam A, Kennedy GC, Kita D, Labat
thkowitz D, Pot D, Randazzo F, Re
, Sudduth-Klinger J, Williams LT;
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                                                                 and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue typing; profiling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giese K, L. Giese K, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n products which cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reinhard
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Sequence 1454 BP;

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                                                                                                                                            1240 CACTNTNCGCCNCCTCGCNCCGCNCNNNCCCCGCCACGCANACANNGCATCNNCACCTCC 1181
                                                                                                                                                                                                                                                                                                                    1180 GCGTCCCCCACACGNGACCAGCCCNCNCNCNAANCACCNGCNGTCNGCNCTNCCACC 1121
                                                                                                                                                                                                                                                                                                                                                                1120 ACACCCACCCCCCCCCCCCCCCNCNCNCCCCATCCTCGGNCACCCTANNNNCCNCACACGC 1061
                                                                                                                 tggcccgctacgcccagcgggtcatggactggctacaccccgacggcgacctcaccgaca 190
                                                         caccegecaggeegeegaageegaectgeeggeaaaggeeteaatategteeegaegage 130
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                      1420 CCCNCNGCNCGCGCCCACACCCACNCACACCCCNACCCCCCNTCCNCCCGCCCCCNNCGTC
                                                                                                                                                                                           251 getaagtggetacetgacceccaagtcgcgggccacetttgaagccgtgctagccaaac
                                                                                                                                                                                                                                                                                                                                                    191 ccgaacgcgcccgcaaacgcgcatcaccctgagcaaccagcaatacgacggcatgtcacg
                                                                                                                                                                                                                                                                                            tggccgcccccggcgcgaccaaccccgacgaccacacc-ccggtcatcgacaccacccc
Length 1454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human genes and their expression products which are
Score 47.2; DB 20; Length
Pred. No. 0.099;
0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones ML, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1060 CCCNCACNGCGCCGCACNC 1042
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98US-0072910.
98US-0075954.
98US-0080114.
                                                                                                                                                                                                                                                                                                                                                                                                            430 ctggccgggctgcgcgcg 448
 10.48;
40.48;
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                               Conservative
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                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9938972-A2
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03-APR-1998
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ1253 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ1233 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polynuchisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polyncleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer,
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; Mismatches 296;
differentially expressed in different cell types
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                                                                                                                           Claim 1; Page 2250-2251; 2479pp; English.
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Search completed: April 2, 2002, 22:49:09 Job time: 9209 sec

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Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 33, Appli Sequence 7, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli

Sequence 1, Sequence 1, Sequence 1,

Title:

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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,727
REPERENCE/DATET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
US-09-320-878-22

US-07-705-490-1

US-08-455-073A-1

US-08-455-073A-1

US-08-105-537-3

US-08-105-537-3

US-08-105-537-3

US-08-105-537-3

US-08-105-537-3

US-08-112-138

US-09-430-886-6

US-09-430-854-7

US-09-312-038-4

US-09-312-038-3

US-09-312-038-3

US-09-312-038-3

US-09-312-038-3

US-09-312-038-3

US-09-312-038-3

US-08-37-428-1
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97.8%; Pred. No. 3.3e-80;
iive 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                   US-08-439-009A-1
                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 18M PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08464052
; Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-08-464-052-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPRANE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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Best Local Similarity 97.8
Matches 446; Conservative
            double
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STATE: New York
COUNTRY: U.S.A.
  TYPE: nucleic STRANDEDNESS:
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Sequence 5
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                                                                           April 3, 2002, 05:46:33 ; Search time 165.4 Seconds
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                       Compugen Ltd
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4 US-08-461-002-1
4 US-08-469-411-1
5 PCT-US94-09863-1
3 US-08-390-878-18
3 US-08-390-878-18
4 US-08-461-002-5
4 US-08-461-052-5
4 US-09-103-8408-2
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US-08-418-200-1
US-08-428-745-1
US-08-444-083-6
US-08-442-145-6
US-08-443-1245-6
US-08-443-130-6
US-08-898-911-6
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US-09-105-537-15
             GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES TITLE OF INVENTION: THEREOF WUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                   1126 GTGCTAGCCAAACTGGCCGCCCCGGCCGGACCAACCCGGACCACACCCCGGTCATC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1186 GACACCCCCGGATGCGGCCGCCATCGACGCGACCCGCAGCCAACGCAAC 1245
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon, Hargrave, Devans & STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/689,41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-689-411-1; Sequence 1, Application US/08689411; Patent No. 6224881; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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   Conservative
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CLASSIFICATION: 536
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: U.S.A.
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                                                                                    ACGGCATGTCACGGCTAAGTGGCTACCTGACCCCCCAAG-CGCGGGCCACCTTTGAAGCC 1125
                                                                                                                                                                                                  tggatgtgtccacccgccaggccgccgaagccgacctgccggcaaaggc--ctcaatatc 118
                                                                    gtecegaegagetggeeegetaegeeeagegggteatggaetggetaeaeeeeegaeggeg
                                                                                                                                                                                                                                                                                                                                       gacaccacccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 408.4; DB 4
Pred. No. 3.3e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                          1246 CACGACGGCTGCTGGCCGGCTGCGCCGCCTGATC 1281
                                                                                                                                                                                                                                                                                                                                                                                                      418 cacgacgggctgctggccgggctgcgcgctgatc 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon, Hargrave, Devans & STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/461,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08461002
; Patent No. 6214543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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97.8%;
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STRANDEDNESS: double
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ZIP: 14603
COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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: U.S.A.
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US-08-461-002-1
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Query Match
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                                                                                                                     4;
                                                                                       Length 1535;
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TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR
TITLE OF INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
                                                                                                                  9
                                                                                  Score 408.4; DB 4
Pred. No. 3.3e-80;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1246 CACGACGCCTGCTGGCCGGCTGCGCCGCCTGATC 1281
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OORRESPONDENCE ADDRESS:
ADDRESSE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9409863 GENERAL INFORMATION:
         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                    Query Match 90.2%;
Best Local Similarity 97.8%;
Matches 446; Conservative
STRANDEDNESS:
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                                        US-08-689-411-1
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238 acqgcatqtcarqqctaaylggctacctgaccccaagtcgcgggccacctttgaaqcr 297
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WEN'ER, John C.
TITLE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULÓSIS
FILE REFERENCE: 24366-2007:00
CURRENT APPLICATION UNIMBER US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
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                                                                                                                                                                              Length 1535;
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Pred. No. 3.3e-80;
0; Mismatches 6;
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    Sequence 1, Application US/05103840A
    Patent No. 629433
    GENERAL INFORMATION;

                            SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                          90.2%;
TELEFAX: (716)-263-1600 INFORMATION FOR SEQ ID NO:
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SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 1
                                                                                                                                                                                                          Conservative
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CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                        Similarity
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                                                                                                                                                                       Query Match
Best Local Simil
Matches 446; C
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PCT-US94-09863-1
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Length 4411529;

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DB

Score 408.4;

90.28;

us-09-785-904-2.rni

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Db 1789400 TGGATGTCTCCACCCGCCAGGCCGCCGACCTGGCCGGCAAAGCCGCTCAATATC 1789341
                                                                                                                                                                                                     'n
                                                                           Db 1789460 GAICGCCGAGGCGCACGCACGTCAAAGTGATTGCGCCCTTTTTTGCCCCACCTGCCGCGGG 1789401
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                           4; Gaps
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APPLICANT: Stored, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREFT: One Market Plaza, Steuart Street Tower, 20th
STREFT: California
COUNTRY: USA
                     Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/ACENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1789041 CACGACGGCTGCTGCCGGGCTGCGCGCGCTGATC 1789006
97.8%; Pred. No. 6.6e-80;
Live 0; Mismatches 6;
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Patent No. 5700683
GENERAL INFORMATION:
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NAME: HUNCEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,543,9600
TELEPAX: 415,543,5043
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SEQUENCE CHARACTERISTICS:
LENGTH: 12412 base pairs
TYPE: nucleic acid
Best Local Similarity 97.8
Matches 446; Conservative
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
                                                                                                                                                                                             361
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                                                                                       Length 12412;
                                                                                                                12; Indels
                                                                                       DB 1;
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PatentIn Release #1.0, Version #1.25
                                                                                     Score 366.8; DB 1
Pred. No. 3.7e-71;
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                                                                                                               0; Mismatches
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CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
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Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1BM PC compatible
                            DNA (genomic)
                                                                                 Query Match
Best Local Similarity 95.6%;
Matches 432; Conservative
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CORRESPONDENCE ADDRESS:
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-390-878-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14603
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ADDRESSEE:
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: Up
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                              gacctcaccgacaccgaacgcgcccgcaaacgc-gcatcaccctgagcaaccagcaatac 236
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                                                                                                                                                                     Length 650;
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STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PIB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                    77.5%; Score 351; DB 3; 97.7%; Pred. No. 7.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccacgacggctgctggccgggctgcgcgcgctgatc 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08461002 Patent No. 6214543
                                                   LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-464-052-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
(716) 263-1304
         TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   Best Local Similarity 97.7
Matches 388; Conservative
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                                                                                                                                                                     Query Match
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DNA MOLECULE FRAGMENTS ENCODING FOR CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
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                                                                                                                                                                                                                                                                   Length 650;
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OPERATING SYSTEM: PC-DOS/NNS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doyle LLF
                                                                                                                                                                                                                                                                 Score 351; DB 4;
Pred. No. 7.2e-68;
0; Mismatches 5,
   19603/186 (D-1485B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Nixon, Hargrave, Devans & Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squeence 5, Application US/080894111
Fateri No. 6224081
GENERAL, INFORMATION:
APPLICANT: Kiley H.D., Lee W.
APPLICANT: Clong, Pede
TITLE OF INVENTION: CELLULAR UPTAK
TITLE OF INVENTION: CELLULAR UPTAK
TITLE OF SEQUENCES: HEREOF
MUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     0;
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                    ; 'TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-5
                                                                                                                                                                                                                                                             77.58;
97.78;
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                                                                                                              LENGTH: 650 base pairs
TYPE: nucleic acid
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   Matches 388; Conservative
                                                                                                                                                STRANDEDNESS: double
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CITY: Rochester
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APPLICANT: Pan, Yang
TITLE OF INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/05201
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
SEALIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: REALSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
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Pred. No. 7.2e-68;
O; Mismatches 5;
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09128155
Patent No. 6117654
                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-689-411-5
                                                                                       TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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97.78;
            ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                  LENGTH: 650 base pairs
TYPE: nucleic acid
STKANDEDNESS: double
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Best Local Similarity 97.7'
Matches 388; Conservative
CLASSIFICATION: 536
                                                                                                                                                                                                 unknown
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ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WASSER, Claire M.
APPLICANT: VENTURE, John C.
TITLE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: UNERTHOUSIS
TITLE OF INVENTION: UNERTHOUSIS
CHERENTE: 14 444, 20007, 00
CHERENT APPLICATION UNBERT 15/09/103,840A
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                                                                                                                                                Length 152331;
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                                                                                                                                        11.6%; Score 52.4; DB 3;
ilarity 45.6%; Pred. No. 0.003;
Conservative 0; Mismatches 217;
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Pred. No. 0.018;
0; Mismatches
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; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or
US-09-128-155-16
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98.0%;
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
US-09-103-840A-2
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SEQ ID NO 2
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Matches 447; Conservative
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                                                                                                                                      Query Match
Best Local Similarity
Matches 182; Conserv
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Db 3870029 acggtatgtcacggctaagtggctacctgacccccaag-cgcgggccacctltqaaqcc 3870087
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               tgjatgtgtccaccgccaggcgcgaagccgacctgccggcaaaggc--ctcaatatc 118
                                                                                                                                                179 aceteacegacacegaacgegecegeaacge-geateaceetyageaaceageatacg 237
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97.1%; Pred. No. 0.027;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN; TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various
; OTHER INFORMATION: represent a, t, c or
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium tuberculosis
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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APPLICANT: Toupet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTIONS STAUCOSPORIN BIOSYNTHESIS Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1996-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
FARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%; Score 44.6; DB 4; Length 6085;
51.2%; Pred. No. 0.11;
99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptomyces longisporoflavus
                                                                                                                                     Sequence 4, Application US/09029603 Patent No. 6210935
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nes 104; Conservative
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalic
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LOCATION: (1747)..(2553)
OFHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCAFION: (5071)..(6085)
OTHER INFORMATION: ORF
.09-029-603-4
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OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_KNA
LOCATION: (2593)..(
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LOCATION: (4013)..(
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RESULT 15
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Db 3883955 tggatgtgtccacccgccaggccgacgacctgyccggcaaagccgctcaatatc 3884014

      QY
      179 acctcaccgacaccgaacgcccgcaaacgc-gcatcaccctgagcaaccagcaatacg 237

      Db
      3884075 acctcaccgacaccgaacgcgccgcaaacgcggcatcaccctgagcaaccagcaatacg 3884134

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 3884135 acggcatgtcacggctaagtggctacctgacccccaay-cgcgggccacctttgaagcc 3884193
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Db 3884254 gacaccacccccgatgcggccgcatcgaccgcgacacccgcagccaacgcaac 3884313
                    5418 ggtcgaggcggtcaccgaacgcacccgctgcctgctcccggtccacctgtacggcca 5477
                                                                                      119 gtoccgacgaggctggcccgctacgcccagcggqtcatggactggctacaccccqacqgcq 178
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FURTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNDERR: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 acggcatgtcacggctaagtggctacctgacccccaagtcgcgggccacctttgaagcc 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
309 actggccgccccggcgcgaccaaccccgacgaccacaccccggtcatcgacaccaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.6; DB 4; Length 4411529;
Pred. No. 0.32;
0; Mismatches 6; Indels 4; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                   5478 gtgcgtcgacatggcgccgctga 5500
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                                                                                                                                                                         429 gctggccgggctgcgcgctga 451
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APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity 97.8
Matches 446; Conservative
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LENGTH: 4411529
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US-09-103-840A-1
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280 egggceacctttgaagcegtgctagceaaactggcegceccegggeggaceaeccegae 339
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Pred. No. 0.17;
0; Mismatches 76;
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                                                                                                                                                                                                                               APPLICANT: LYNCH, Michael
TITLE OF INVENTION: DNA SEQUENCES RELAT
TITLE OF INVENTION: FRAGILE X SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10,113
RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6600
                                                                                                                                                                            MULLEY, John C
MANDEL, Jean-Louis
PRITCHARD, Melanie April
LYNCH, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/638,518
FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/118,200
09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/672,232 FILING DATE: 20-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 0S 07/966,517 FILING DATE: 23-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                      RICHARDS, Kobert I
SCHLESSINGER, David
NAGARAJA, Kamaiah
KREMEK, Eric J
Sequence 1, Application US/08118200
Patent No. 6197500
                                                     SUTHERLAND, Grant R
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crane Fearty, Sharon E
                                                                                                                                              YU, Sni
BAKEK, Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-202J
INCEMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 53.9%;
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                  GENERAL INFORMATION:
APPLICANT: SUTHER
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US-08-118-200-1
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APPLICANT:
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APPLICANT:
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Search completed: April 3, 2002, 08:04:13 Job time: 42013 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: April 2, 2002, 21:47:49; Search time 3835.7 Seconds (without alignments) 1269.087 Million cell updates/sec</pre>	
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US-09-785-904-2 453 1 gatcggcgaggcgcacatca.....ccgggctgcgcgctgatc 453 Title: Perfect score:

Scoring table: Sequence:

11351937 seqs, 5372889281 residues IDENTITY\_NUC Gapoxt 1.0 Searched:

22703874 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

em\_gss\_inv: \*
em\_gss\_pln: \*
em\_gss\_pro: \*
em\_gss\_rod: \*
em\_gss\_vrt: \*
em\_gss\_other: \* gb\_gss:\* em\_gss\_tun:\* em\_gss\_hum:\* em\_estfun:\*
em\_estfun:\*
em\_estfun:\*
em\_estpl:\*
em\_estpl:\*
em\_estpo:\*
em\_estpo 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AL057121 Drosophil AL104440 Drosophil BG786264 SEAUMCO06 AL104349 Drosophil BG241147 OVI\_38\_G1 AL520271 Tetraodon AL053013 Drosophil AL108460 Drosophil AL393518 T7 end of BG3320266 Zm03\_G3g0 AL537183 AL537183 AZ211117 SP\_0159\_B Description CNS0057B CNS014PA BG786264 CNS016264 BG241147 CNS027YE CNS017SY CNS06D94 ALS320266 ALS32031B3 ID 13 113 113 113 113 113 Query Match Length DB 1014 11101 576 11101 520 848 925 11101 644 632 13.5 112.8 112.7 112.5 112.5 112.4 112.4 55 56 56 56 56 56 56 56 56 Score 4 5 6 7 7 8 8 9 11 11 12 Result ĕ.

AZ200928 SP_0134_B A2196321 SP_1031 B		7	0	_			5	~	7	_	0	AZ194728 SP 1028_B	0			AL525224 AL525224			4				SP 100		æ			~		. (	2
AZ200928 AZ196321	CNS03JN0	CNS010RY	CNS0118A	CNS006B4	CNS004NB	BG368625	BG786339	CNS015VV	BG413362	BC786337	AZ046300	AZ194728	BG076530	CNS0071A	B09456	AL525224	CNS04CNH	CNS006XK	AZ185894	CNS015AB	A2184272	AZ194927	A2185516	AZ188474	CNS02R43	CNS03LU9	CNS0181P	A2195437	AL581447	CNS00720	CNS0155J
13	13	13	13	13	13	11	11	13	11	11	13	13	11	13	13	10	13	13	13	13	13	13	13	13	13	13	13	13	10	13	13
892 786	266	176	848	806	839	1016	878	1038	631	999	745	892	669	895	978	666	549	935	794	1028	673	741	775	795	802	1016	1101	915	925	932	1059
12.3	12.2	ς.		ς.		12.1		12.1	12.0	12.0	12.0	_	Η,	11.8	11.8	11.8	11.7	11.7	11.7	11.6	11.6	11.6	11.6	11.6						11.5	11.5
55.8	55.4	S	S	ď.	52	S	4	٠	4			m	۳.	۳.	e.	۳.	m.	53			52.4	52.4	52.4	52.4		52.4		52.2		52.2	52.2
13	15	16	17	18	19	20	21	22	23	24	25	97	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5
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## ALIGNMENTS

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Similarity
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                                                                              Matches 136;
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                                                Query Match
                                                                 Local
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LOCUS
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KEYWURDS
SOURCE
ORGANISM
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre of Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-JUL-1999) Genoscope · Centre National de Sequencage :
BP 191 91006 EVRY cedex · FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence "7 end of BAC BACNIZMIA of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                   aagtggctacctgacccccaagt/gcgggccacctttgaagccgtgctagccaaactgg 313
                                                                                                                                                                                                                                                                                                                                                                                     MCMCMCCMCCCCCCGMCAACCCMYCCCCMGCMTMMCMCCGCCTMCCMMMCMCTC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                 cogcocooggogogaccaaccccgacgaccacaccccggtcatcgacaccccccgaty 373
                                                                                                                                                                                                                                       134 eccyctacycccaycygytcatygactyyctacaccccyacygcyacctcaccyacaccy 193
                                                                                                                                                                                                                                                                    164 SMCCCCSCCCCSMACSCCCAMSACCCGCCMGAMTCCMAGTCSCGATCCTCCCTCCCGTSM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 CCMMCCSCCCMCCCCMCMCCMCCCMCCMCCSMCCGCMCCTCCMCCTCCCGGCCTC 403
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly.
Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inserta;
Eukaryota; Neoptera; Endopleryqotu; Diptera; Brachytera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                           Length 1014;
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                                                                                                                                                                        13.5%; Score 61.2; DB 13; Length ilarity 35.9%; Pred. No. 0.014; Conservative 57; Mismatches 120; Indels
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/plasmid="pbeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN12M14"
                               melanogaster"
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                                                                                                            168
                          /organism="Drosophila m./db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11K11"
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Bukaryota, Merdazda, Berlinodermata; Eleutherozoa; Echinozoa;
Echinoidea, Buechinoidea: Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 576)
2bu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. an Elleuschu, C.A.
A larae scale analysis of mRNAs expressed by primary mescuchyme cells of the sea urefuln embryo.
Development 128 (2001) In press
                                                                                               70 ccacccgcraggccgccgaagccgaccgaccgacaaggcctcaatatcgtccrgacgaq 129
                                                                                                                                                                                                 130 etggecegniacynnoagngggtratygactgyctacacceegaeggegaeeteanegan 189
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Length 1101;
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                                                   Indels
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4400 Fitth Avenue, Pittsburgh, PA 15213, USA
TTEL: it 1412 268 5849
Email: cttensohn∜andrew.emu.edu.
  DB 13;
                                              52; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="PC_0028_A2_B05_MR"/clone_lib="Sea urchin primary
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                    Pred. No. 0.028;
13.2%; Score 59.6; 38.7%; Pred. No. 0.0
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Drosophila melanogaster genome survey sequence T7 end of BAC
BA. 11214 of DrosBAC library from Drosophila melanogaster (fruit
fl ), genomic survey sequence.
AL104949
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                                                              cccacctgcccgccgcggtggatgtgtccacccgccaggccgccgaagccgacctgccgg 102
                                                                                       caaaggeeteaatategteeegaegagetggeeegetacgeeeagegggteatggaetgg 162
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                                  Gaps
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    Length 576;
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
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   DB 11;
Score 58.2; DB 11;
Pred. No. 0.05;
0; Mismatches 220;
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/clone="BACN12114"
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 12.8%;
Query Match 12.8
Best Local Similarity 45.8
Matches 186; Conservative
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/note="Organ: Mix of ovaries of varying immature stayes
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Fanicoideae; Andropogoneae; Sorghum.
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Cordonice Praff,M. M., Ginqle,A., Marsala,C., Sudman,M. and Praff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An ESF database from Sorghum: ovaries of varying immature stages Unpublished (2000)
Contact: Cordonnier-Praft MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG241147 520 bp mkNA EST 15-FEB-206 0V1_38_G10.bl_A002 Ovary 1 (OV1) Sorghum bicolor cDNA, mRNA sequence.
BG241147
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                                                                                                                                                                                                                                                                                                                                                                                                                                0;
     Length 1101;
                                                  Indels
Score 57.4; DB 13;
Pred. No. 0.075;
25; Mismatches 188;
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12.78;
42.08;
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                    Best Local Similarity 42.0%
Matches 154; Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSO2YYE 848 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
181307 of library G from Tetraodon nigroviridis, genomic survey
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GSS: genome survey sequence.
Tetraodon nigrovitridis.
Tetraodon nigrovitridis
Tetraodon nigrovitridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Tetraodontidae; Tetraodon.
Tetraodontidae; Tetraodon.
I (bases I to 848)
Roest-Crollius H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Weissenbach,J.
from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision." 233\ {\rm c} 113 g 59\ {\rm t}
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                              205 aaacgcgcatcaccctgagcaaccagcaatacgacggcatgtcacgggtaagtggctacc
                                                                                                                                                                                                                                                                                                                                                                                             265 tgacccccaagtcgcgggccacctttgaagccgtgctagccaaactggccgccccggc
                                                                                                                                                                               0;
                                                                                                                                   Length 520;
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                                                                                                                            Score 56.8; DB 11;
Pred. No. 0.093;
0; Mismatches 167;
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48.5%;
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Best Local Similarity 48.59
Matches 157, Conservative
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FEATURES

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Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY ccdex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley brosophila Genome Project (BDCP).

The BDCP is constructing a physical map of the brosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDCP prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Plater de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 ctggccgcrcccgqcgqcgaccaacccgaccacacccggtcatcgacacraccccc 369
                                                                                                                                                                                                                            10 ggcycacatraaaglgattcgcgcccttttcgcccacctgcccgcgggggggggtggt 69
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Nooptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:99883"
/clone="18107"
/clone_"15p="G"
/note="Genoscope sequence ID : COAC
                                                                                                         34
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                                                                                                                                                                Score 56.6; DB 13;
Pred. No. 0.1;
5; Mismatches 209;
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Genoscope.

United (13-70L-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                  511 others
                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/rolone="BACRI9D16"
/note="end: TET3"
61 c 61 g 172 t 511
                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
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11.8%; Pred. No. 0.1
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Plasmid Drosophila melanogaster
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TY end of clone ARGAANHDL2 of Hibrary ARGAA from strain CBS 732
Zygosaccharamycas rouxil, genemic survey sequence.
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
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O
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                                                                                                                                                 359 others
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                               /organism="Drosophila melanogaster"
/Plasmid="pBeloHAC11"
/Plasmid="taxon:7227"
/Clone_lib="DrosbAC"
/Clone="BACN471.08"
/Inote="end : SP6"
4 a 176 c 160 y 152 r 359 ot!
                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                              Score 56.4; DB 13;
Pred. No. 0.12;
4; Mismatches 155;
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FEBS Lett. 487 (1), 52-55 (2000)
20584718
     Location/Qualifiers
                                                                                                                                                                                                   Query Match
Best Local Similarity 14.4%; Pro
Matches 57; Conservative 184;
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                                                                                 Direct Submission

As Submitted (06-SEP-2000) Genoscope - Centre National de Sequencade,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

Seqreféqenoscope.cns: fr - Neb: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii; Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

Location/Qualifiers
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1 (bases 1 to 632)
Simmonds,J.A., Singh,J.A., Piche,C., Cass,L., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D.
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yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56.2; DB 13;
Pred. No. 0.12;
4; Mismatches 112;
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/clone="AR0AA011D12"
/clone_lib="AR0AA"
/note="end : T7"
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35.78;
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Best Local Similarity 35.7
Matches 92; Conservative
                                                                     Genoscope
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/clone_lib="zm03_a0801"
/clone_lib="zm03_aAFC_ECORC_cold_stressed_maize_seedlings"
/clone_lib="zm03_aAFC_ECORC_cold_stressed_maize_seedlings"
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/clone_stage="4-leaf"
/clone_vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
/clo_stage="vector: Bluescript SK+/XhoI-EcoRI; Site_2: Xho I; Corn seedlings at 4-leaf stage were exposed to low temperature/high light (looc/700-800uE/m2/s) for 4 days. Plants were grown/treated by J. Simmonds/L. Cass.
Library prepared by C. Piche using Stratagene kit."
a 326 c 85 g 67 t 52 Others
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  Tags from Cold-Stressed Maize Seedlings Grown
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
             Under High Light Intensity
Unpublished (2001)
Contact: Singh,J.A.
Bastern Cereal and Oilseed Research Centre
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA OC6, Canada
Fax: (613) 759-1662
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AL537183 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSOBF019YL14
prime, mRNA sequence.
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Mismatches 166; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56;
Pred. No. (
                                                                                                                                                                                                                                                                                     /cultivar-"C0328"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                /organism="Zea mays"
                                                                                                                                                                                                                        Location/Qualifiers
Sequence Tags fro
Light Intensity
                                                                                                                                                                                          Email: singhja@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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EST.
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Matches 137; Conservative
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High quality sequence stop: 921.
                                                                                                                                                                                                                                                                                                                                                                                                Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 159 row: F column: 9
Seq primer: SP6
Class: BAC ends
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47.78;
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Matches 190; Conservative
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                                                                                                                                                                                                                                                                                                                                           /lab_nost="Delta" of week)
//lab_nost="Delta" of week)
//note="Organ: Fetal brain; Vector: pcMvSPORT 6: 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
pcMvSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
// Maryland 20850, USA Fax: (1) 301 610 8371 Email:
http://fulllength.invitrogen.com"
                                                                                                                                                                  /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Lil_F013_FBrn1"
/clone_lib="Li
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                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 egegecettttegeceacetgecegeegeggtggatgtgtecaceegeeaggeega
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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; AZ200928 892 bp DNA GSS 31-AUG-2000 SP\_0134\_B2\_C12\_T7A Strongylocentrotus purpuratus, purple sea urchin , sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-134 Col=24 Row=F, DNA sequence. and Strongylocentrotidae: Strongylocentrotus.

1 (bases 1 to 921)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. ar Hood, I. 53 egocgogytogatglytocaccegroaggocycogaagcogacctgcoggoaaaggecto 112 233 alachachardaleachgelaastigacetgaceccaagtegeagecacettq 292 353 teatequeuecacecegatgegyreyeategaecquagaeaecageageeageeaag 173 anggogannteanngaeanngaangnyngengaaangngeateacetgageancagea A sea urchin genome project: Sequence scan, virtual map, additional resources Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000) 20402566 Contact: Cameron, RA, Davidson, EH, Hood, L ;; Length 921; others 1. 921 /organism-"Strongylocentrotus purpuratus 207; Indels Davidson, EH, Hood, L Score 56; DB 13; Pred. No. 0.14; 0; Mismatches 207; gcaaccardacqqctqctgqccqqqctgcqcgctg 450 27 t Division of Biology 156-29 California Institute of Technology

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ACCESSION

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DB 13; Length 786;
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida;
Strongylocentrolidae; Strongylocentrotus.
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Fred, No. 0.16;
0; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Division of Biology 156-29
California Institute of Technology
Basadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 786 Location/Qualifiers
                                                                                                                                                                            Strongylocentrotus purpuratus.
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: acameron@caltech.edu
                                                                                                                                          AZ196321.1 GI:8390144
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/db_xref="taxon:766"

/clone="Plate="134 Col=24 Row=F"

/clone="Plate="34 Col=24 Row=F"

/clone="lb="Strongylocentrotus purpuratus, purple sea

/rochin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli

DH10B"
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Cameron, R. A., Mahairas, G., Rast, J. P., Martinez, P., Biondi, T. R.,
Swartzell, S., Wallace, J. C., Poustka, A. J., Livingston, B. T., Wray
, G. A., Ettensohn, C. A., Lehrach, H., Britten, R. J., Davidson, E. H. and
Hood, L.
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                                                                                                                                                                                                  A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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                                                               Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
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California Institute of Technology Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 55.8; DB 13;
llarity 46.0%; Pred. No. 0.15;
Conservative 0; Mismatches 222;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Email: acameron@caltech.edu
Plate: 134 row: F column: 24
Seq primer: T7
                                                  Strongylocentrotus purpuratus.
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                 GI:8395946
                                                                                                                                                                                                                                                                                                                                                    Tel: (626) 395-8421
Fax: (626) 793-3047
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AZ196721 786 bp DNA GSS 31-AUG-2000 SP\_1031\_B2\_D02\_T7A Strongylocentrotus purpuratus, purple sea urchin sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-1031 Col-4 KOW-H, DNA sequence. /db\_xrei-"(axon:77668"
/db\_xrei-"(axon:77668"
/clone-"Plate-1031 Col=4 Row-H"
/clone-lib-"Strongylocentrotus purpuratus, purple sea
urchin, sperm gunomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli ï (bases 1 to 786)

Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swattzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lohrach, H., Britten, R.J., Davidson, E.H. and Hood, L. 50 georgeography and 1919 technological georga ageoga of 1909 acquired and 1009 acquired and 1009 acquired and 1009 acquired and 1009 acquired acqu ctdaatairqtcrogacgagotggnoogotacgoccayogggtcatggactggotacard 169 230 gcaalacgae-ggcalglcacggclaaglggclacclgacccccaaglcgcgggccarc 288 ccgacggryacctcaccgacaccgaacgccccgcaacgcgcatcaccctgagcaacra 229 349 coggicalingacaccaccecegatgegececategacegegacecegeagecagecaager 408 Gaps Echinozoa; A sea urchin genome project: Sequence scan, virtual map, additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000) 20402566 .; δ

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GSS: genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis.

Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha: Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

E 1 (bases 1 to 566)

S Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,

Meissenbach,J. Billault,A., Quetler,F., Saurin,W., Bernot,A. and

Charaterization and repeat analysis of the compact genome of the
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                      566 bp DNA GSS 17-MAY-2000 nigroviridis genome survey sequence PUC-Ori end of clone library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizanes, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using retraction nigroviridis DNA sequence
121 cccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacggcgac 180
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/db_xref="taxon:99883"
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/clone="1bb="G"
/note="Genoscope sequence ID : COBG031DA02sPl-end
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Best Local Simil
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